

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds  
(without alignments)  
3290.816 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708

Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGWNFSVNGSGSVIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_nhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirts.\*  
16: sp\_bacteriap.\*  
17: sp\_archeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2409	89.0	516	2	O82839
2	1942	71.7	533	2	O9A054
3	1934	71.4	513	16	O81X74
4	1926	71.1	513	16	O81A54
5	1889.5	69.8	613	2	O59222
6	1874	69.2	519	2	O9RQ78
7	1872.5	69.1	549	2	O31193
8	1867.5	69.0	521	2	P71034
9	1867.5	69.0	549	2	O9KW6
10	1813.5	67.0	501	2	O93148
11	1576.5	58.2	507	16	O87HG6
12	1363	50.3	493	2	O3657
13	1336	49.3	481	16	O89YF1
14	1307.5	48.3	486	16	O8DT08
15	1307.5	48.3	488	16	O8E0M2
16	1300.5	48.0	488	16	O8E696

#### ALIGNMENTS

RESULT 1

O82839 PRELIMINARY; PRT; 516 AA.  
AC O82839; DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Amylase.  
OS Bacillus sp.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1409;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-KSM-1378;  
RK MEDLINE=96342096; PubMed=9675143;  
RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T., Ozaki K., Ito S.;  
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of an arginine-glycine residue is caused by enhanced calcium binding.";  
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).  
DR EMBL; AB008763; BAA32431.1; -;  
DR HSSP; P06278; 1VJS.  
DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha\_amyl\_cat.  
DR InterPro; IPR006589; Alp\_amyl\_cat\_sub.  
DR Pfam; PF00128; Glyco\_hydro\_13.  
DR PRINTS; PR00128; alpha-amylase; 1.  
DR SMART; SM00642; Amy; 1.  
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 89.0%; Score 2409; DB 2; Length 516;

Best Local Similarity 86.0%; Pred. No. 5.9e-143;

Matches 417; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWYLPNDGHNHNRILRSDASNLKDKGISAVWIPPAWKGSQNDVGYGA 60

Db 32 HHNGTNGTMQYFEWYLPNDGHNHNRILRSDASNLKDKGISAVWIPPAWKGSQNDVGYGA 91

Q97Q49 streptococ  
Q8DPC8 streptococ  
Q8YUZI anabaena sp  
Q68875 streptococ  
O50593 streptococ  
Q53786 streptococ  
Q9G59 lactococcus  
Q8U916 agrobacteri  
Q8Z585 salmonella  
Q8XBB6 escherichia  
Q8FGL8 escherichia  
Q7UAB0 shigella fl  
Q83Z40 shigella fl  
Q877B1 aspergillus  
O33476 pyrococcus  
Q8NKR4 thermococcu  
Q8NKR5 thermococcu  
O50200 thermococcu  
Q9P910 pyrococcus  
O08452 pyrococcus  
Q8U319 pyrococcus  
Q8JZK3 uncultured  
O93647 thermococcu  
Q60051 thermococcu  
Q7X9T1 phaseolus a  
Q42678 cuscutoa ref  
Q60224 natronococ  
Q8LJQ6 musa acumin  
Q8LP27 pharbitis n

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QY 61. YDLYDI-GEFNOKGRTIRTKYGTNRNOLQAAYVALKSNGLIYVGVVMMHKGADATMVRVAV 120  
 Db YDLYDI-GEFNOKGRTIRTKYGTNRNOLQAAYVALKSNGLIYVGVVMMHKGADATMVRVAV 151  
 QY 121. EVNPNRNOEVSSEYITIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYK 180  
 Db EVNPNRNOEVSSEYITIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYK 211  
 QY 181. RGGKGDWDEVDTEGNGYDLYMADIMDHPVNNELRWGVMYTNLTGLDGFRIDAVKH 240  
 Db RGGKGDWDEVDTEGNGYDLYMADIMDHPVNNELRWGVMYTNLTGLDGFRIDAVKH 271  
 QY 241. IKYSFTDMWLNHVSATGKMFVAEFAWFKNDLGAENYLNKTNWNSVDFVPLHYNLNA 300  
 Db IKYSFTDMWLNHVSATGKMFVAEFAWFKNDLGAENYLNKTNWNSVDFVPLHYNLNA 331  
 QY 301. SKSGGNYDMROIENGTVQRPMPHVAITFVDNHDSPQEEALESFVEWFKPLAYALTLTRE 360  
 Db SKSGGNYDMROIENGTVQRPMPHVAITFVDNHDSPQEEALESFVEWFKPLAYALTLTRE 391  
 QY 361. QYPSVFGDYGYGIPTHGVPMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 420  
 Db QYPSVFGDYGYGIPTHGVPMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 451  
 QY 421. HNSGLATIMSDGAGGNKMFVGRNKAQGVWTDITGNRAGTGTITNADGWNFSVNGSGVS 480  
 Db HNSGLATIMSDGAGGNKMFVGRNKAQGVWTDITGNRAGTGTITNADGWNFSVNGSGVS 511  
 QY 481. IWVK 485  
 Db 512 VVVKQ 516

RESULT 2  
 Q9AQ54  
 ID Q9AQ54 PRELIMINARY; PRT; 533 AA.  
 AC Q9AQ54;  
 DT 01-JUN-2001 (TREMELrel. 17, Created)  
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
 DE Alpha-amylose.  
 OS Bacillus megaterium.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1404;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,  
 Park K.-H.;  
 RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium  
 KSM B-404";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF220440; AAK00598.1; --  
 DR HSSP; P06278; 1VJS.  
 DR GO; GO:0004556; P:alpha-amylose activity; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR006047; Alpha\_aml\_cat.  
 DR InterPro; IPR006589; Alp\_aml\_cat\_sub.  
 DR Pfam; PF00128; alpha-amylose; 1.  
 DR SMART; SM00642; Amy; 1.  
 SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 71.7%; Score 1942; DB 2; Length 533;  
 Best Local Similarity 69.6%; Pred. No. 1.1e-113;  
 Matches 336; Conservative 57; Mismatches 86; Indels 4; Gaps 2;  
 QY 6 NGTMMQYFENYLPDNGNHNRLSDASNLKDGISAWIPPAWKGASQNDVGAYDLYD 65  
 Db NGTMMQYFENYLPDNGNHNRLSDASNLKDGISAWIPPAWKGASQNDVGAYDLYD 111  
 QY 66 LGSEFNOKGRTIRTKYGTNRNOLQAAYVALKSNGLIYVGVVMMHKGADATMVRVAVNPN 125  
 Db LGSEFNOKGRTIRTKYGTNRNOLQAAYVALKSNGLIYVGVVMMHKGADATMVRVAVNPN 171

QY 126. NRNEQVSSEYITIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKPRGDGK 185  
 Db NRNEQVSSEYITIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKPRGDGK 230  
 QY 186. GHDWEVDTEGNGYDLYMADIMDHPVNNELRWGVMYTNLTGLDGFRIDAVKHYSF 245  
 Db GHDWEVDTEGNGYDLYMADIMDHPVNNELRWGVMYTNLTGLDGFRIDAVKHYSF 290  
 QY 246. TRDMWLNHVSATGKMFVAEFAWFKNDLGAENYLNKTNWNSVDFVPLHYNLNAKSGG 305  
 Db TRDMWLNHVSATGKMFVAEFAWFKNDLGAENYLNKTNWNSVDFVPLHYNLNAKSGG 350  
 QY 306. NYDMRQIENGTVQRPMPHVAITFVDNHDSPQEEALESFVEWFKPLAYALTLTREOGYPS 365  
 Db NYDMRQIENGTVQRPMPHVAITFVDNHDSPQEEALESFVEWFKPLAYALTLTREOGYPS 410  
 QY 366. VYGYDYGI---PTHGVPMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTAHP 422  
 Db VYGYDYGI---PTHGVPMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTAHP 470  
 QY 423. NSGLATIMSDGAGGNKMFVGRNKAQGVWTDITGNRAGTGTITNADGWNFSVNGSGVS 482  
 Db NSGLATIMSDGAGGNKMFVGRNKAQGVWTDITGNRAGTGTITNADGWNFSVNGSGVS 530  
 QY 483. VNK 485  
 Db 531 VQR 533

RESULT 3  
 Q81YJ4  
 ID Q81YJ4 PRELIMINARY; PRT; 513 AA.  
 AC Q81YJ4;  
 DT 01-JUN-2003 (TREMELrel. 24, Created)  
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Alpha-amylose.  
 GN AMYS OR BA3551.  
 OS Bacillus anthracis (strain Ames).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=198094;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22608414; PubMed=12721629;  
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,  
 Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,  
 Holtzapple E.K., Okstad O.A., Helgason E., Rinkac L.M., Gwinn M.,  
 Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,  
 DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
 Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,  
 Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,  
 Thomson B., Friedlander A.M., Koshler T.M., Hanna P.C., Kolsto A.-B.,  
 Fraser C.M.;  
 RT "The genome sequence of Bacillus anthracis Ames and comparison to  
 closely related bacteria";  
 RL Nature 423:81-86(2003).  
 DR EMBL; AB017035; AAP27311.1; --  
 DR TIGR; BA3551; --  
 DR GO; GO:0004556; P:alpha-amylose activity; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR006047; Alpha\_aml\_cat.  
 DR InterPro; IPR006589; Alp\_aml\_cat\_sub.  
 DR Pfam; PF00128; alpha-amylose; 1.  
 DR SMART; SM00642; Amy; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 71.4%; Score 1934; DB 16; Length 513;  
 Best Local Similarity 69.4%; Pred. No. 3.4e-113;  
 Matches 335; Conservative 59; Mismatches 85; Indels 4; Gaps 2;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds  
(without alignments)  
3290.816 Million cell updates/sec

Title: US-09-925-576C-2

Perfect score: 2714

Sequence: 1 HHNGTNGTMQYFEWILPND.....ADGHWGNSVGGSVVWVKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP\_TREMBL\_25;\*  
2: sp\_archaea;\*  
3: sp\_bacteria;\*  
4: sp\_fungi;\*  
5: sp\_human;\*  
6: sp\_invertebrate;\*  
7: sp\_mammal;\*  
8: sp\_mhc;\*  
9: sp\_organelle;\*  
10: sp\_phase;\*  
11: sp\_plant;\*  
12: sp\_rodent;\*  
13: sp\_virus;\*  
14: sp\_vertebrate;\*  
15: sp\_unclassified;\*  
16: sp\_rvirus;\*  
17: sp\_bacteriap;\*  
18: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2613	96.3	516	2	082839
2	1962	72.3	513	16	Q81YJ4 bacillus sp
3	1956	72.1	513	16	Q81A54 bacillus ce
4	1956	72.1	533	2	Q9AQS4 bacillus me
5	1947.5	71.8	613	2	Q59222 bacillus sp
6	1918	70.7	519	2	Q9QRT8 cytophaga s
7	1907.5	70.3	549	2	Q31193 bacillus st
8	1902.5	70.1	521	2	P71034 bacillus sp
9	1902.5	70.1	549	2	Q9KMY6 bacillus st
10	1835.5	67.6	501	2	Q93148 bacillus sp
11	1544.5	56.9	507	16	Q87H66 vibrio para
12	1344	49.5	493	2	Q03657 bacillus ci
13	1329	49.0	481	16	Q89YF1 bacteroides
14	1274.5	47.0	486	16	Q8DT08 streptococc
15	1259.5	46.4	488	16	Q8EOM2 streptococc
16	1256.5	46.3	488	16	Q8E696 streptococc

17	1245	45.9	484	16	Q97Q49
18	1243	45.8	484	16	Q8DPC8
19	1239	45.7	492	16	Q8YU21
20	1235.5	45.5	486	2	Q68875
21	1223.5	45.1	484	2	Q50583
22	1205.5	44.4	485	2	Q53786
23	1127	41.5	491	16	Q9CG59
24	1097	40.4	506	16	Q8U916
25	1066	39.3	494	16	Q8Z5S5
26	1054	38.8	495	16	Q8XBB6
27	1054	38.8	495	16	Q8FGL8
28	1047	38.6	495	16	Q7UAB0
29	1045	38.5	495	16	Q83R40
30	1011.5	37.3	529	3	Q877B1
31	475.5	17.5	461	1	Q8NKR4
32	473.5	17.4	461	1	Q33476
33	470	17.3	469	1	O50200
34	469.5	17.3	460	1	Q9P9L0
35	469.5	17.3	460	1	O08452
36	469.5	17.3	473	17	Q8U319
37	460	16.9	461	1	Q8NKR5
38	451	16.6	432	14	Q8JZK3
39	447	16.5	457	1	O93647
40	303	11.2	416	10	Q8LJQ6
41	303	11.2	424	10	Q8LP27
42	300.5	11.1	421	10	Q7X9T1
43	298	11.0	420	10	Q9ZP43
44	295.5	10.9	482	2	Q60051
45	292	10.8	416	10	Q8GUR0

#### ALIGNMENTS

#### RESULT 1

ID O82839 PRELIMINARY; PRT; 516 AA.  
AC O82839;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Amylase.  
OS Bacillus sp.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1409;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KSM-1378;  
RX MEDLINE=98342096; PubMed=9675143;  
RA Igarashi K., Hatada Y., Ikawa K., Azaki H., Ozawa T., Kobayashi T.,  
RA Ozaki K., Ito S.;  
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of  
RT an arginine-glycine residue is caused by enhanced calcium binding.";  
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).  
DR EMBL; AB008763; BAA32431.1; -;  
DR HSSP; P06278; 1VJS.  
DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha\_aml\_cat.  
DR InterPro; IPR006589; Alp\_aml\_cat\_sub.  
DR InterPro; IPR006046; Glyco\_hydro\_13.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR PRINTS; PR00110; ALPHAMYLASE.  
DR SMART; SM00642; Amy; 1.  
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 96.3%; Score 2613; DB 2; Length 516;

Best Local Similarity 95.1%; Pred. No. 4.1e-161;

Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWILPNDGHNHNRLLRDDAANLKSIGITAVWIPPAWKGTQNDVGYGA 60

Db 32 HHNGTNGTMQYFEWILPNDGHNHNRLLRDDAANLKSIGITAVWIPPAWKGTQNDVGYGA 91



QY 61 YDLYLDFEFGNKGTVRTKYGTRNLOQAATSLKNGIQVYGDVVMNHKGADGTEIYNAV 120  
 Db 92 YDLYLDFEFGNKGTVRTKYGTRNLOQAATSLKNGIQVYGDVVMNHKGADGTEIYNAV 151  
 QY 121 EVNRSNRNQTSGEYATIAEATWTKFDFPGRGNHSHSFKRWYHFDGTDQSRQLQNKIYKF 180  
 Db 152 EVNRSNRNQTSGEYATIAEATWTKFDFPGRGNHSHSFKRWYHFDGTDQSRQLQNKIYKF 211  
 QY 181 RGTGKAWDEVDTEGNYDYLYMYADVDMDHPEVIELRNWGVWYTNLNLDFGFRIDAVKH 240  
 Db 212 RGTGKAWDEVDTEGNYDYLYMYADVDMDHPEVIELRNWGVWYTNLNLDFGFRIDAVKH 271  
 QY 241 IKYFTDRLWTHVRNTTGKPMFAVAEFKNDLGALENYLNKTSNNHSHFVDFVPLHNYLYNA 300  
 Db 272 IKYFTDRLWTHVRNTTGKPMFAVAEFKNDLGALENYLNKTSNNHSHFVDFVPLHNYLYNA 331  
 QY 301 SNSGGYIDMRNLINGSVVOXKHPHVAFTFVDNHDSPQGEALSFVQOWFKPLAYALVLTRE 360  
 Db 332 SNSGGYIDMRNLINGSVVOXKHPHVAFTFVDNHDSPQGEALSFVQOWFKPLAYALVLTRE 391  
 QY 361 QGYPSVFYGDYIGYPTGHPVPMKSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTRGNS 420  
 Db 392 QGYPSVFYGDYIGYPTGHPVPMKSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTRGNS 451  
 QY 421 HPNSGLATIMSDGPGGNKMWYGVKNKAGOVWREDITGNRTGTVTINADGWNFSVNGSGVS 480  
 Db 452 HPNSGLATIMSDGPGGNKMWYGVKNKAGOVWREDITGNRTGTVTINADGWNFSVNGSGVS 511  
 QY 481 VVVKQ 485  
 Db 512 VVVKQ 516

## RESULT 2

Q81YJ4 ID Q81YJ4 PRELIMINARY; PRT; 513 AA.  
 AC Q81YJ4;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Alpha-amylase.  
 GN AMYS OR BA3551.  
 OS Bacillus anthracis (strain Ames).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=198094;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22608414; PubMed=12721629;  
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,  
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,  
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,  
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkak L.M., Gwinn M.,  
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman J.C.,  
 RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,  
 RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,  
 RA Fraser C.M.;  
 RT "The genome sequence of Bacillus anthracis Ames and comparison to  
 RT closely related bacteria."  
 RL Nature 423:81-86(2003).  
 DR EMBL; AE017035; AAP27311.1; --  
 DR TIGR; BA3551;  
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR006047; Alpha amyl cat.  
 DR InterPro; IPR006589; Alp amyl cat\_sub.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR SMART; SM00642; Amy; 1.  
 DR Complete proteome.  
 DR KN  
 DR SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 72.3%; Score 1962; DB 16; Length 513;  
 Best Local Similarity 70.2%; Pred. No. 5.6e-119;  
 Matches 339; Conservative 63; Mismatches 77; Indels 4; Gaps 2;

QY 6 NGTMMQYFEMYLFPDNGNHNRLRDDAANLKSXGTAIVTIPPAWKGTSONDVGAYGAYDLYD 65  
 Db 32 NGTMMQYFEMYLFPDNGNHNRLRDDAANLKSXGTAIVTIPPAWKGTSONDVGAYGAYDLYD 91  
 QY 66 LGFENQKGVTRKYGTRNLOQAATSLKNGIQVYGDVVMNHKGADGTEIYNAVENVRS 125  
 Db 92 LGFENQKGVTRKYGTRNLOQAATSLKNGIQVYGDVVMNHKGADGTEIYNAVENVRS 151  
 QY 126 NNRQETSGEYATIAEATWTKFDFPGRGNHSHSFKRWYHFDGTDQSRQLQNKIYKRGCTOK 185  
 Db 152 NNRQETSGEYATIAEATWTKFDFPGRGNHSHSFKRWYHFDGTDQSRQLQNKIYKRGCTOK 210  
 QY 186 AWDWEVDTEGNYDYLYMYADVDMDHPEVIELRNWGVWYTNLNLDFGFRIDAVKHICYSF 245  
 Db 211 AWDWEVDTEGNYDYLYMYADVDMDHPEVIELRNWGVWYTNLNLDFGFRIDAVKHICYSF 270  
 QY 246 TRDMLTHVRNTTGKPMFAVAEFKNDLGALENYLNKTSNNHSHFVDFVPLHNYLYNASNSGG 305  
 Db 271 TRDMLTHVRNTTGKPMFAVAEFKNDLGALENYLNKTSNNHSHFVDFVPLHNYLYNASNSGG 330  
 QY 306 YDMRNILINGSVVOXKHPHVAFTFVDNHDSPQGEALSFVQOWFKPLAYALVLTREOGYPS 365  
 Db 331 YDMRNILINGSVVOXKHPHVAFTFVDNHDSPQGEALSFVQOWFKPLAYALVLTREOGYPS 390  
 QY 366 VFYGDYIGYPTGHPVPMKSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTRGNSHP 422  
 Db 391 VFYGDYIGYPTGHPVPMKSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTRGNSHP 450  
 QY 423 NSGLATIMSDGPGGNKMWYGVKNKAGOVWREDITGNRTGTVTINADGWNFSVNGSGVSVM 482  
 Db 451 NSGLATIMSDGPGGNKMWYGVKNKAGOVWREDITGNRTGTVTINADGWNFSVNGSGVSVM 510  
 QY 483 VKQ 485  
 Db 511 VQO 513

## RESULT 3

Q81AS4 ID Q81AS4 PRELIMINARY; PRT; 513 AA.  
 AC Q81AS4;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Glucan 1,4-alpha-maltonhexaoidase (EC 3.2.1.98).  
 GN BC3482.  
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=226900;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22608415; PubMed=12721630;  
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,  
 RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,  
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,  
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,  
 RA Overbeek R., Kyrpides N.;  
 RT "Genome sequence of Bacillus cereus and comparative analysis with  
 RT Bacillus anthracis."  
 RL Nature 423:87-91(2003).  
 DR EMBL; AE017009; AAP10417.1; --  
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
 DR GO; GO:0016798; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR006047; Alpha amyl cat.  
 DR InterPro; IPR006589; Alp amyl cat\_sub.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR SMART; SM00642; Amy; 1.  
 DR Complete proteome.  
 DR KN  
 DR SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46:501 Seconds  
(without alignments)  
3290.816 Million cell updates/sec

Title: US-09-925-576C-2

Perfect score: 2714

Sequence: 1 HHNGTGTMMQYFEWYLPND.....ADGWNFSVNGSVVWKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2613	96.3	516	2	O82839
2	1962	72.3	513	16	O81YJ4
3	1956	72.1	513	16	O81AS4
4	1956	72.1	533	2	O9A054
5	1947.5	71.8	613	2	O59222
6	1918	70.7	519	2	O9ROT8
7	1907.5	70.3	549	2	O31193
8	1902.5	70.1	521	2	P71034
9	1902.5	70.1	549	2	O9KWY6
10	1835.5	67.6	501	2	O93148
11	1544.5	56.9	507	16	O87HG6
12	1344	49.5	493	2	O03657
13	1329	49.0	481	16	O89YI1
14	1274.5	47.0	486	16	O8DT08
15	1259.5	46.4	488	16	O8E0M2
16	1256.5	46.3	488	16	O8E696

## ALIGNMENTS

### RESULT 1

O82839 PRELIMINARY; PRT; 516 AA.

AC O82839.  
BT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Amylase.

OS Bacillus sp.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1409;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=KSM-1378;

RX MEDLINE=98342096; PubMed=9675143;

RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,

RA Ozaki K., Ito S.;

RT "Improved thermostability of a Bacillus alpha-amylase by deletion of

an arginine-glycine residue is caused by enhanced calcium binding.";

RL Biochem. Biophys. Res. Commun. 248:372-377(1998).

DR EMBL; AB008763; BAA32431.1; -

DR HSSP; P06278; 1VJS.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; InterPro:IPR006047; Alpha\_amyl\_cat.

DR InterPro; InterPro:IPR006589; Alp\_amyl\_cat\_sub.

DR Pfam; PF00128; Glyco\_hydro\_13.

DR PRINTS; PR00128; alpha-amylase; 1.

DR SMART; SM00642; Amy; 1.

SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 96.3%; Score 2613; DB 2; Length 516;

Best Local Similarity 95.1%; Pred. No. 4.1e-161;

Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSGITAVWIPPAWKGTSDNDVGYGA 60

Db 32 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSGITAVWIPPAWKGTSDNDVGYGA 91

Q97Q49 streptococ  
Q8DPC8 streptococ  
Q8YU21 anabaena sp  
Q68875 streptococ  
Q50583 streptococ  
Q53786 streptococ  
Q9C959 lactococcus  
Q8U916 agrobacteri  
Q8Z585 salmonella  
Q8XBB6 escherichia  
Q8FGL8 escherichia  
Q7UAB0 shigella fl  
Q83440 shigella fl  
Q877B1 aspergillus  
Q8NKR4 thermococcu  
Q33476 pyrococcus  
Q50200 thermococcu  
Q9P910 pyrococcus  
Q08452 pyrococcus  
Q8U319 pyrococcus  
Q8NKR5 thermococcu  
Q8JZK3 uncultured  
Q33647 thermococcu  
Q81YJ4 musa acumin  
Q81P27 pharbitis n  
Q7X9T1 phaseolus a  
Q9ZP43 phaseolus v  
Q60051 thermoactin  
Q8GUR0 musa acumin

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QY 61 YDLGFBFNGQGTVRTKYGTNRNLOAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
Db 92 YDLGFBFNGQGTVRTKYGTNRNLOAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 151
QY 121 EVNRSNRNOETSGEYAIENAWTKFDPGGRNHHSSFKRWYHFDGTDWDSQOLQNKIYKF 180
Db 152 EVNRSNRNOETSGEYAIENAWTKFDPGGRNHHSSFKRWYHFDGTDWDSQOLQNKIYKF 211
QY 181 RGTGKAWDEVDTENGNDYLMYADVDMDHPEVTHELRNMGVWYTNLTNLGDFRIDAVKH 240
Db 212 RGTGKAWDEVDTENGNDYLMYADVDMDHPEVTHELRNMGVWYTNLTNLGDFRIDAVKH 271
QY 241 IKYSTROWLTHVRNTTGKMPFAVAEFAWKNDLGAENYLNKTSNNHVSFVDFVPLHYNLYNA 300
Db 272 IKYSTROWLTHVRNTTGKMPFAVAEFAWKNDLGAENYLNKTSNNHVSFVDFVPLHYNLYNA 331
QY 301 SNSGGYVDMRNILNGSVVQKHPHTAVTFVNDHDSQPGEALESFVQOQFKPLAYALVLTRE 360
Db 332 SNSGGYVDMRNILNGSVVQKHPHTAVTFVNDHDSQPGEALESFVQOQFKPLAYALVLTRE 391
QY 361 QGYPSVFYGGYGTPTGCVPAKMSKIDPLLOAROTFAYGTDHDFDHDHIIIGWTREGNSS 420
Db 392 QGYPSVFYGGYGTPTGCVPAKMSKIDPLLOAROTFAYGTDHDFDHDHIIIGWTREGNSS 451
QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGSGVS 480
Db 452 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGSGVS 511
QY 481 VVVKQ 485
Db 512 VVVKQ 516

RESULT 2
Q81V74 ID Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4;
OC NCBI_TaxID=198094;
RN [1]
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzaple E.K., Ostad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Clime R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
DR EMBL; AB017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;
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Query Match 72.3%; Score 1962; DB 16; Length 513;
Best Local Similarity 70.2%; Pred. No. 5.6e-119;
Matches 339; Conservative 63; Mismatches 77; Indels 4; Gaps 2;

QY 6 NGTMMQYFEWYLPNDGNHNRLLDDAANLKSIGTAVTWPAPWKGTSQNDVGYGAYDLYD 65
Db 32 NGTMMQYFEWYLPNDGNHNRLLDDAANLKSIGTAVTWPAPWKGTSQNDVGYGAYDLYD 91
QY 66 LGFENQGTVRTKYGTNRNLOAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAVNR 125
Db 92 LGFENQGTVRTKYGTNRNLOAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAVNR 151
QY 126 NRNOETSGEYAIENAWTKFDPGGRNHHSSFKRWYHFDGTDWDSQOLQNKIYKF 185
Db 152 NRNOETSGEYAIENAWTKFDPGGRNHHSSFKRWYHFDGTDWDSQOLQNKIYKF 210
QY 186 ANDWEYDTENGNDYLMYADVDMDHPEVTHELRNMGVWYTNLTNLGDFRIDAVKH 245
Db 211 ANDWEYDTENGNDYLMYADVDMDHPEVTHELRNMGVWYTNLTNLGDFRIDAVKH 270
QY 246 TRDMLTHVRNTTGKMPFAVAEFAWKNDLGAENYLNKTSNNHVSFVDFVPLHYNLYNA 305
Db 271 TRDMLTHVRNTTGKMPFAVAEFAWKNDLGAENYLNKTSNNHVSFVDFVPLHYNLYNA 330
QY 306 YDMRNILNGSVVQKHPHTAVTFVNDHDSQPGEALESFVQOQFKPLAYALVLTRE 365
Db 331 YDMRNILNGSVVQKHPHTAVTFVNDHDSQPGEALESFVQOQFKPLAYALVLTRE 390
QY 366 VYGYDYGI---PTHGVPAMSKIDPLLOAROTFAYGTDHDFDHDHIIIGWTREGNSSHP 422
Db 391 VYGYDYGI---PTHGVPAMSKIDPLLOAROTFAYGTDHDFDHDHIIIGWTREGNSSHP 450
QY 423 NSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGSGVS 482
Db 451 NSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGSGVS 510
QY 483 VVVKQ 485
Db 511 VVVKQ 513

RESULT 3
Q81AS4 ID Q81AS4; PRELIMINARY; PRT; 513 AA.
AC Q81AS4;
OC NCBI_TaxID=226900;
RN [1]
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Gallerton N., Candelon B.,
RA Kapral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AB017009; AAP10417.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Complete proteome.
```

```
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BFF9F6 CRC64;

Query Match
Best Local Similarity 72.1%; Score 1956; DB 16; Length 513;
Matches 340; Conservative 58; Mismatches 81; Indels 4; Gaps 2;

QY 6 NGTMQYFEWYLPNDGNHNRRLRDAANLKSIGTAVMIPPAWKGTSONDVGAYDLYD 65
DB 32 NGTLNQYFEWYLPNDGNHNRRLRDAANLKSIGTAVMIPPAWKGTSONDVGAYDLYD 91
QY 66 LGFENQKGTVRTKTYGTNRQAAVTSLNKNGIQYGVDMVNMHKGADTEIVNAVEVNR 125
DB 92 LGFENQKGTVRTKTYGTNRQAAVTSLNKNGIQYGVDMVNMHKGADTEIVNAVEVNR 151
QY 126 NRNETSGEVAIEAWTKFDPGRGNHSSFKRWYHFDGTDWDSROLQNKIYKFRGTGK 185
DB 92 LGFENQKGTVRTKTYGTNRQAAVTSLNKNGIQYGVDMVNMHKGADTEIVNAVEVNR 210
QY 186 AWDHEVDTEGNNGYDLYMAYADVDMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHISYF 245
DB 211 AWDHEVSENGYDLYMAYADVDMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHISYF 270
QY 246 TRDLWTHVRNTTKPMFAVAEFAWKNDLGAENYLNKTSWHSVDFVPLHYNLNASGG 305
DB 271 LRDMVNVHVRQOTGKEMFTVAEYQNDIQTLNNYLAKVYNSQSVFADPLHYNFHYASTGNG 330
QY 306 YYDMRNILNSVQKHPHTAVTFVDNHDSPGEALSFVQOQKPLAYALVLTREQVPS 365
DB 331 NYDMRNILKGTVANHPTLAVTLVENHDSQPQSLESVSPWPKLAYAFILTRAEGVPS 390
QY 366 VFYGDYGI---PTHGVPAMKSKIDPLLOARQTFAYGTQHDYDFDHHDIIGWTRGNSHP 422
DB 391 VFYGDYGI---PTHGVPAMKSKIDPLLOARQTFAYGTQHDYDFDHHDIIGWTRGNSHP 450
QY 423 NSGLATIMSDPGGNKMWYGVKNKAGQVWRDITGNRTGTITNADGNGFVNSGVSVM 482
DB 451 NSGLATIMSDPGGNKMWYGVKNKAGQVWRDITGNRTGTITNADGNGFVNSGVSVM 510
QY 483 VKQ 485
DB 511 VQ 513

RESULT 4
Q9AQ54
ID Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT KSM B-404";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match
Best Local Similarity 72.1%; Score 1956; DB 2; Length 533;
Matches 339; Conservative 61; Mismatches 79; Indels 4; Gaps 2;

QY 6 NGTMQYFEWYLPNDGNHNRRLRDAANLKSIGTAVMIPPAWKGTSONDVGAYDLYD 65
DB 52 NGTLNQYFEWYLPNDGNHNRRLRDAANLKSIGTAVMIPPAWKGTSONDVGAYDLYD 111
QY 66 LGFENQKGTVRTKTYGTNRQAAVTSLNKNGIQYGVDMVNMHKGADTEIVNAVEVNR 125
DB 112 LGFENQKGTVRTKTYGTNRQAAVTSLNKNGIQYGVDMVNMHKGADTEIVNAVEVNR 171
QY 126 NRNETSGEVAIEAWTKFDPGRGNHSSFKRWYHFDGTDWDSROLQNKIYKFRGTGK 185
DB 172 NRNEVSGDYEISAWTKFDPGRGNHSSFKRWYHFDGTDWDSROLQNKIYKFRGTGK 230
QY 186 AWDHEVDTEGNNGYDLYMAYADVDMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHISYF 245
DB 231 AWDHEVSENGYDLYMAYADVDMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHISYF 290
QY 246 TRDLWTHVRNTTKPMFAVAEFAWKNDLGAENYLNKTSWHSVDFVPLHYNLNASGG 305
DB 291 LRDMVNVHVRQOTGKEMFTVAEYQNDIQTLNNYLAKVYNSQSVFADPLHYNFHYASTGNG 350
QY 306 YYDMRNILNSVQKHPHTAVTFVDNHDSPGEALSFVQOQKPLAYALVLTREQVPS 365
DB 351 NYDMRNILKGTVANHPTLAVTLVENHDSQPQSLESVSPWPKLAYAFILTRAEGVPS 410
QY 366 VFYGDYGI---PTHGVPAMKSKIDPLLOARQTFAYGTQHDYDFDHHDIIGWTRGNSHP 422
DB 411 VFYGDYGI---PTHGVPAMKSKIDPLLOARQTFAYGTQHDYDFDHHDIIGWTRGNSHP 470
QY 423 NSGLATIMSDPGGNKMWYGVKNKAGQVWRDITGNRTGTITNADGNGFVNSGVSVM 482
DB 471 NSGLATIMSDPGGNKMWYGVKNKAGQVWRDITGNRTGTITNADGNGFVNSGVSVM 530
QY 483 VKQ 485
DB 531 VQ 533

RESULT 5
Q59222
ID Q59222 PRELIMINARY; PRT; 613 AA.
AC Q59222;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.2.1).
GN AMY.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RA Lin L.-L., Chu W.S., Hsu W.H.;
RA STRAIN=TS-23;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22045; AAA63900.1; -.
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat_sub.
DR InterPro; IPR002044; CBD 4.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD 4; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
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SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;

Query Match 71.8%; Score 1947.5; DB 2; Length 613;  
Best Local Similarity 70.3%; Pred. No. 6.1e-118; Indels 1; Gaps 1;  
Matches 336; Conservative 66; Mismatches 75;

QY 6 NGTMMQYFEWYLPNDGNHNRDLDDAANLKSKGITAVWIPPAWKGTSDNDVGYGAYDLYD 65  
DB 36 NETMMQYFEWYLPNDGNLTDAPYLSVGITAVWTPPAYKGTSDNDVGYGAYDLYD 95

QY 66 LGSEFNQKGTVRTKYGTRNQLQAATVSLKNNGIQVYGDVVMNHKGGADGTEIVNAVEVNR 125  
DB 96 LGSEFNQKGTVRTKYGTRNQLQAATVSLKNNGIQVYGDVVMNHKGGADGTEIVNAVEVNR 155

QY 126 NNRQETSSEYAIKAWTKFDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKFRGTG 185  
DB 156 NNRQETSSEYAIKAWTKFDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKFRGTG 214

QY 186 AWDWEVDTEGNYDYLMDHPEVIHELNRWGVYVNTNLNLDGFRIDAVKHIKYSF 245  
DB 215 AWDWEVDTEGNYDYLMDHPEVIHELNRWGVYVNTNLNLDGFRIDAVKHIKYSF 274

QY 246 TRDMLTHVRNTGKPMFAVAFKNDLGAENLNTKSNHSDVDPVPLHNLNNAASGG 305  
DB 275 FPDWLTIVRNQTKNLFVAGFWSYDVKLNHITTKNGSMFLDAPLHNNFYTASKSSG 334

QY 306 YDWMENILNGSVQKHPHTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTREQGYP 365  
DB 335 YDWMENILNGSVQKHPHTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTREQGYP 394

QY 366 VFYGDYGGIPTHGVPAKMSKIDPLLOARQTFAYGTQHDYFDHHDIIIGWTREGNSHPNSG 425  
DB 395 VFYGDYGGIPTHGVPAKMSKIDPLLOARQTFAYGTQHDYFDHHDIIIGWTREGNSHPNSG 454

QY 426 LATIMSDGPGGNKMWYGVKNGAGVWRDITGNRTCTVTINADGWNFSVNGSSVSU 483  
DB 455 LATIMSDGPGGNKMWYGVKNGAGVWRDITGNRTCTVTINADGWNFSVNGSSVSU 512

RESULT 6

ID Q9RQT8 PRELIMINARY; PRT; 519 AA.

AC Q9RQT8  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Raw starch digesting amylase precursor.  
OS Cytophaga sp.  
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;  
OC Flexibacteraceae; Cytophaga.  
OX NCBI\_TaxID=29535;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jeang C.L., Chen L.S., Chen M.Y.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF067653; AAF00567.1; -  
DR HSSP; P06278; 1VJS.  
DR GO; GO:0004556; P:alpha-amylase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha\_amy1\_cat.  
DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR PRINTS; PR00110; ALPHAMYLASE.  
DR SMART; SM00642; Amy; 1.  
KW Signal.  
FT SIGNAL  
FT CHAIN  
SQ SEQUENCE 519 AA; 58337 MW; 3B6B88A4DF98B163 CRC64;

Query Match 70.7%; Score 1918; DB 2; Length 519;  
Best Local Similarity 69.2%; Pred. No. 4e-116; Indels 4; Gaps 2;  
Matches 335; Conservative 67; Mismatches 78;

QY 5 TNGTMMQYFEWYLPNDGNHNRDLDDAANLKSKGITAVWIPPAWKGTSDNDVGYGAYDLY 64  
DB 37 TNGTMMQYFEWYLPNDGQNNLRDTPAYLSVGITAVWTPPAYKGTSDNDVGYGAYDLY 96

QY 65 DLGEFNQKGTVRTKYGTRNQLQAATVSLKNNGIQVYGDVVMNHKGGADGTEIVNAVEVNR 124  
DB 97 DLGEFNQKGTVRTKYGTRNQLQAATVSLKNNGIQVYGDVVMNHKGGADGTEIVNAVEVNR 156

QY 125 SNRNETSSEYAIKAWTKFDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKFRGTG 184  
DB 157 SNRNETSSEYAIKAWTKFDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKFRGTG 215

QY 185 KAWDEVDTEGNYDYLMDHPEVIHELNRWGVYVNTNLNLDGFRIDAVKHIKYS 244  
DB 216 KAWDEVDTEGNYDYLMDHPEVIHELNRWGVYVNTNLNLDGFRIDAVKHIKYS 275

QY 245 FTRDMLTHVRNTGKPMFAVAFKNDLGAENLNTKSNHSDVDPVPLHNLNNAASGG 304  
DB 276 FLKDWYDNRATGKEMFTVGEYQNDLGAENLNTKSNHSDVDPVPLHNLNNAASGG 335

QY 305 GYDWMENILNGSVQKHPHTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTREQGYP 364  
DB 336 GYDWMENILNGSVQKHPHTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTREQGYP 395

QY 365 SVFYGDYGGIPTHGVPAKMSKIDPLLOARQTFAYGTQHDYFDHHDIIIGWTREGNSH 421  
DB 396 SVFYGDYGGIPTHGVPAKMSKIDPLLOARQTFAYGTQHDYFDHHDIIIGWTREGNSH 455

QY 422 PMSGLATIMSDGPGGNKMWYGVKNGAGVWRDITGNRTCTVTINADGWNFSVNGSSVSU 481  
DB 456 AKSGLATIMSDGPGGNKMWYGVKNGAGVWRDITGNRTCTVTINADGWNFSVNGSSVSU 515

QY 482 WVKQ 485  
DB 516 WVKQ 519

RESULT 7

ID Q31193 PRELIMINARY; PRT; 549 AA.

AC Q31193  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Alpha amylase.  
GN AMI.  
OS Bacillus stearothermophilus.  
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.  
OX NCBI\_TaxID=1422;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF032864; AAB86961.1; -  
DR PIR; A54541; A54541.  
DR HSSP; P06278; 1VJS.  
DR GO; GO:0004556; P:alpha-amylase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha\_amy1\_cat.  
DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR PRINTS; PR00110; ALPHAMYLASE.  
DR SMART; SM00642; Amy; 1.  
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

Query Match 70.3%; Score 1907.5; DB 2; Length 549;  
Best Local Similarity 68.6%; Pred. No. 2.1e-115; Indels 1; Gaps 1;  
Matches 328; Conservative 70; Mismatches 79;



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39 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSDVGYGYDLYD 98
66 LGFENQKGTVRTKYGTRNQLQAAVTSLKNGIOYQYGDVVMNHKGGADGTEIVNAVEVNR 125
99 LGFENQKGTVRTKYGTRKQAQYLQIAAAHAAGMAYADVDFDHKGGADGTEWDAVEVNP 158
126 NRQNETSGEYAEIAEWTKFDPGRGNHSSFKRWYHFDGTDWDSRKL-SRIYKFRGIGK 185
159 DRNQEISGTQIQAWTKFDPGRGNTYSSFKRWYHFDGTDWDSRKL-SRIYKFRGIGK 217
186 AWDWEVDTENGNDYLMAYADVMDHPEVIELHNRWGVYNTNLDGFRIDAVKHKYSF 245
218 AWDWEVDTENGNDYLMAYADVMDHPEVIELHNRWGVYNTNLDGFRIDAVKHKYSF 277
246 TRDMLTHVRNTGKPMFAVAFWKNDLGAENYLNKTSWNHSDVPDVLPHYNLNASNGG 305
278 FPDWLSVRSQTGKPLFTVGEYMSYDINKLHNYITKTNGTMSLDPADLHNFYTASKSG 337
306 YYDMRNILNGSVVQKHPHTHVAFTVDNHDSDGPEALESFVQWFKPLAYALVLTREQYPS 365
338 AFDMRTLMTNTLMKDQPTLAVTFVDNHDTPGQALQSWDPWFKPLAYAFILTRQEGYPC 397
366 VFYGDYIGIPTHGVPAKMSKIDPLLOAROTFAYGTQHDYFDHDIIGWTREGNSHNSG 425
398 VFYGDYIGIPTHGVPAKMSKIDPLLOAROTFAYGTQHDYFDHDIIGWTREGVTEKPGSG 457
426 LATIMSDPGCGNKMVYGVKQAGVWRDITGNRTGTVTINADGWNFSVNGSVVWV 483
458 LAALITDGPCKGKMWYGVKQAGVYDITGNRSDTITNSDGMGEFKVNGSVVWV 515

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## RESULT 8

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P71034
ID P71034 PRELIMINARY; PRT; 521 AA.
AC O9KMY6;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
RT thermostable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005375; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596022E1 CRC64;

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Query Match 1 34 POTENTIAL.
Best Local Similarity 35 521 ALPHA-AMYLASE.
Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;
6 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSDVGYGYDLYD 65
39 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSDVGYGYDLYD 98

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Qy 66 LGFENQKGTVRTKYGTRNQLQAAVTSLKNGIOYQYGDVVMNHKGGADGTEIVNAVEVNR 125
Db 99 LGFENQKGTVRTKYGTRKQAQYLQIAAAHAAGMAYADVDFDHKGGADGTEWDAVEVNP 158
Qy 126 NRQNETSGEYAEIAEWTKFDPGRGNHSSFKRWYHFDGTDWDSRKL-SRIYKFRGIGK 185
Db 159 DRNQEISGTQIQAWTKFDPGRGNTYSSFKRWYHFDGTDWDSRKL-SRIYKFRGIGK 217
Qy 186 AWDWEVDTENGNDYLMAYADVMDHPEVIELHNRWGVYNTNLDGFRIDAVKHKYSF 245
Db 218 AWDWEVDTENGNDYLMAYADVMDHPEVIELHNRWGVYNTNLDGFRIDAVKHKYSF 277
Qy 246 TRDMLTHVRNTGKPMFAVAFWKNDLGAENYLNKTSWNHSDVPDVLPHYNLNASNGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYMSYDINKLHNYITKTNGTMSLDPADLHNFYTASKSG 337
Qy 306 YYDMRNILNGSVVQKHPHTHVAFTVDNHDSDGPEALESFVQWFKPLAYALVLTREQYPS 365
Db 338 AFDMRTLMTNTLMKDQPTLAVTFVDNHDTPGQALQSWDPWFKPLAYAFILTRQEGYPC 397
Qy 366 VFYGDYIGIPTHGVPAKMSKIDPLLOAROTFAYGTQHDYFDHDIIGWTREGNSHNSG 425
Db 398 VFYGDYIGIPTHGVPAKMSKIDPLLOAROTFAYGTQHDYFDHDIIGWTREGVTEKPGSG 457
Qy 426 LATIMSDPGCGNKMVYGVKQAGVWRDITGNRTGTVTINADGWNFSVNGSVVWV 483
Db 458 LAALITDGPCKGKMWYGVKQAGVYDITGNRSDTITNSDGMGEFKVNGSVVWV 515

RESULT 9
Q9KMY6
ID Q9KMY6 PRELIMINARY; PRT; 549 AA.
AC O9KMY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR GLYCOSIDASE; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CRC64;

Query Match 70.1%; Score 1902.5; DB 2; Length 549;
Best Local Similarity 68.4%; Pred. No. 4.3e-115;
Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;
6 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSDVGYGYDLYD 65
39 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSDVGYGYDLYD 98
Qy 66 LGFENQKGTVRTKYGTRNQLQAAVTSLKNGIOYQYGDVVMNHKGGADGTEIVNAVEVNR 125
Db 99 LGFENQKGTVRTKYGTRKQAQYLQIAAAHAAGMAYADVDFDHKGGADGTEWDAVEVNP 158
Qy 126 NRQNETSGEYAEIAEWTKFDPGRGNHSSFKRWYHFDGTDWDSRKL-SRIYKFRGIGK 185

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159 DB DRNQEISGTYQIAWTKFDPGPRGNTYSSFKRWYHFDGVDWDESRKL-SRIYKPRGIGK 217
186 QY ADWEVDVTENGNDYDLYMADVDMDHPEVIELHRLNWGVVYVNTLNLDFRIDAIVKHIKYSF 245
218 DB ADWEVDVTENGNDYDLYMADVDMDHPEVIELHRLNWGVVYVNTLNLDFRIDAIVKHIKYSF 277
246 QY TRDLWLTHTVRNTTGKPMFAVAEFAEFAEFAEFAEFAEFAEFAEFAEFAEFAEFAEFAE 305
278 DB FPDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKINGTMSLFDAPLHNFYTASKSGG 337
306 QY YDMRNILNGSVVQKHPHTHATVFDVNDHDSQGEALSFVQOQWPKPLAYALVLTREOGYPS 365
338 DB AFDMRTLMTNLTKDQOFTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTROEGYFG 397
366 QY VFYGDYVGIPTGHPVPAKMSKIDPLLOAROTFAYGTOHDYFDHDDIIGWTREGNSHPNSG 425
398 DB VFYGDYVGIPTGHPVPAKMSKIDPLLOAROTFAYGTOHDYFDHDDIIGWTREGVTEKPGSG 457
426 QY LATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTITNADGWGNSFVNGGVSVMV 483
458 DB LAALITDGGPGSKMWYVGNKAGQVWRDITGNRTGTITNADGWGNSFVNGGVSVMV 515

RESULT 10
Q93148
ID Q93148 PRELIMINARY; PRT; 501 AA.
AC Q93148;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
DE AMYK38.
GN AMYK38.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayaishi Y.;
RT "Isolation of a new Bacillus alpha-amylase.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051102; BAB71820.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR Pfam; PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

Query Match 67.6%; Score 1835.5; DB 2; Length 501;
Best Local Similarity 66.3%; Pred. No. 8.4e-111;
Matches 320; Conservative 64; Mismatches 96; Indels 3; Gaps 2;

QY 3 NGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGT-SQNDVGYGAYD 62
DB 22 DGLGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGT-SQNDVGYGAYD 81
QY 63 LYDLGFENQKGTVRTKYGTNRNLQAAVTSLKNGIOVYGDVVMNKHGGADGTEIVNAVEV 122
DB 82 LYDLGFENQKGTVRTKYGTNRNLQAAVTSLKNGIOVYGDVVMNKHGGADGTEIVNAVEV 141
QY 123 NRSNRNQTSGEYIAEAWTKFDPGPRGNNHSSFKRWYHFDGTDWQSRQLQNKIYKFRG 182
DB 142 NPTNRWDISGAYTIDAWTGDFSGRNAYSDFKRWYHFDGTDWQSRQLQNKIYKFRG 200
QY 183 TGKADWEVDVTENGNDYDLYMADVDMDHPEVIELHRLNWGVVYVNTLNLDFRIDAIVKH 242
DB 201 TN--WNRVDEENGNDYDLYMADVDMDHPEVIELHRLNWGVVYVNTLNLDFRIDAIVKH 258
QY 243 YSFTRDLWLTHTVRNTTGKPMFAVAEFAEFAEFAEFAEFAEFAEFAEFAEFAEFAEFAE 302
DB 259 FWTSWVRHQRNEADQDLFVGEYWKDDVGALEFYLDENNWMSLFDVPLNINFRASQ 318
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303 QY SGYYIDMRNILNGSVVQKHPHTHATVFDVNDHDSQGEALSFVQOQWPKPLAYALVLTREOG 362
319 DB QGSGYIDMRNILNGSVVQKHPHTHATVFDVNDHDSQGEALSFVQOQWPKPLAYALVLTREOG 378
363 QY YSFVYGDYVGIPTGHPVPAKMSKIDPLLOAROTFAYGTOHDYFDHDDIIGWTREGNSHP 422
379 DB YFNVFYGDYVGIPTGHPVPAKMSKIDPLLOAROTFAYGTOHDYFDHDDIIGWTREGNSHP 438
423 QY NSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTITNADGWGNSFVNGGVSVMV 482
439 DB NSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTITNADGWGNSFVNGGVSVMV 498
483 QY VKQ 485
499 DB VQ 501

RESULT 11
Q87HG6
ID Q87HG6 PRELIMINARY; PRT; 507 AA.
AC Q87HG6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
DE VPA0999.
GN Vibrio parahaemolyticus.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP05087; BAC62342.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

Query Match 56.9%; Score 1544.5; DB 16; Length 507;
Best Local Similarity 56.9%; Pred. No. 5.8e-92;
Matches 279; Conservative 70; Mismatches 122; Indels 19; Gaps 7;

QY 4 GTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGT-SQNDVGYGAYD 62
DB 24 QNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGT-SQNDVGYGAYD 83
QY 63 LYDLGFENQKGTVRTKYGTNRNLQAAVTSLKNGIOVYGDVVMNKHGGADGTEIVNAVEV 122
DB 84 MYDLGFENQKGTVRTKYGTNRNLQAAVTSLKNGIOVYGDVVMNKHGGADGTEIVNAVEV 143
QY 123 NRSNRNQTSGEYIAEAWTKFDPGPRGNNHSSFKRWYHFDGTDWQSRQLQNKIYKFRG 182
DB 144 DMDNRNIEL-GDKWIEAWVEFNFGPRGNDKYSNFWHTWYHFDGTDWQSRQLQNKIYKFRG 201
QY 183 TGKADWEVDVTENGNDYDLYMADVDMDHPEVIELHRLNWGVVYVNTLNLDFRIDAIVKH 242
DB 202 EGKADWEVDVTENGNDYDLYMADVDMDHPEVIELHRLNWGVVYVNTLNLDFRIDAIVKH 261
QY 243 YSFTRDLWLTHTVRNTTGKPMFAVAEFAEFAEFAEFAEFAEFAEFAEFAEFAEFAEFAE 302
DB 262 YQVLEQWIDHLRWKTKELFTVGEYWKDDVGALEFYLDENNWMSLFDVPLNINFRASQ 321
QY 303 SGYYIDMRNILNGSVVQKHPHTHATVFDVNDHDSQGEALSFVQOQWPKPLAYALVLTREOG 362
```

Db 322 SGGYDMRQIMNGTLMKDNPKAVTLVENHDTQPLQALESTVDMWPKLAFVAFILLREEG 381  
Qy 363 YPSVFGYGYG-----IPTHGVPAKSKIDPQLQAROTFAVGTQHDYFDHDDIIGW 413  
Db 382 YPSVYADYGAQYSDKGYNNMAKVP---YIEELVTLRKEYAYGKQNSYLDHWDVLGW 437  
Qy 414 TREGNSHPNSGLATIMSDGCGNKMVYGNKAGQWRDITGNRTGTVTINADGWNFSV 473  
Db 438 TREGDAEHPNS--MAVIMSDGPGGKWMYTKPSTRYV--DKLGIRTEEVWTDANGWAEFP 494  
Qy 474 VNGGSVSVWV 483  
Db 495 VNGGSVSVWV 504

RESULT 12  
Q03657 PRELIMINARY; PRT; 493 AA.  
AC Q03657; 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Amylase.  
GN AMYE.  
OS Bacillus circulans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1397;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Marcel T.  
RL Nucleic Acids Res. 0:0-0(0).  
DR EMBL; X60779; CAA43194.1; -.  
DR PIR; S15713; S15713.  
DR HSSP; P06278; 1VJS.  
DR GO; GO:0004556; P:alpha-amylase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha amyl cat.  
DR InterPro; IPR006589; Alp amyl cat sub.  
DR Pfam; PF00128; Glyco hydro I3.  
DR PRINTS; PR00128; alpha-amylase; 1.  
DR SMART; SM00642; Amy; 1.  
SQ SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;

Query Match 49.5%; Score 1344; DB 2; Length 493;  
Best Local Similarity 50.9%; Pred. No. 5.3e-79;  
Matches 245; Conservative 75; Mismatches 153; Indels 8; Gaps 3;  
Qy 6 NGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVMIPPAMKGTSDNDVGYGAYDLYD 65  
Db 4 NHTMMQYFEWHLAAGDGHKKLAEMAPELKAKGIDTVWPPVTKAVSAEDTGYGYDLYD 63  
Qy 66 LGEPNQGTVRTKGTTRNQLQAAVTSLNKNGIQYGVGVVNMHKGAGTEIVNAVEVNR 125  
Db 64 LGEPDQGTTRTKGTGTQKQELTEAECQKNGIAYVLDVNMHKGAGDETEVFKVIEVD 123  
Qy 126 NRQETSGEVAIEAWTKFDPGCGNNHSSFKRWYHFDGTDQDSRQLQNKIYKFRGTG 185  
Db 124 DRTKEISEPPEIEGTWTKFTPPGRGDQYSSFKWNSHFNFGTDFD-ARBERTGVFRAGENK 182  
Qy 186 ADWEVDVTENGNDYLMYADVMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHKYSF 245  
Db 183 KWNENVDEFGNDYLMFANIDYHNPDRVREMDWGWKLIDTLCQCGFRDLAKIHNHEP 242  
Qy 246 TRDWLTHVRNTTKGPMFAVAFWKNLDGAIENYLNKTSWNHVSFDPVPLHYNLYNASGG 305  
Db 243 IKEFAEMIRKRGDQFYVGEFNSNLDACREFLDYQIDLDVDSLVHKLHEASLKR 302  
Qy 306 YDMRNTLNSVQKHPTHTAVTFVNDHDSQPGALESFVQGVKPKPLAYALVLTREQYPS 365  
Db 303 DFOLSKIFDPTLVQTHPTHTAVTFVNDHDSQPGALESWIGDWFKPSAYALTLLRRDGY 362

Qy 366 VFYGDYGI-----PTHGVPAKSKIDPQLQAROTFAVGTQHDYFDHDDIIGWREGNSH 421  
Db 363 VFYGDYGI-----KKEILDILLSARCNAKAYGEQEDYFDHANTIGWVRGVEE 419  
Qy 422 ENSGLATIMSDGCGNKMVYGNKAGQWRDITGNRTGTVTINADGWNFSVNGGSV 481  
Db 420 EGSACAVVISNGDDGKRMFGEHRAVEVWDLTKSCDDQITIBEDGWATPHVCGGGSV 479  
Qy 482 W 482  
Db 480 W 480  
RESULT 13  
Q89YF1 PRELIMINARY; PRT; 481 AA.  
AC Q89YF1;  
DT 01-JUN-2003 (Tremblrel. 24, Created)  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Alpha-amylase precursor.  
GN BT4690.  
OS Bacteroides thetaiotaomicron.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VPI-5482 / ATCC 29148;  
RX MEDLINE=22550858; PubMed=12663928;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";  
RL Science 299:2074-2076(2003).  
DR EMBL; AE016946; AA079795.1; -.  
DR GO; GO:0004556; P:alpha-amylase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha amyl cat.  
DR InterPro; IPR006589; Alp amyl cat sub.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR SMART; SM00642; Amy; 1.  
KW Complete proteome.  
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

Query Match 49.0%; Score 1329; DB 16; Length 481;  
Best Local Similarity 49.6%; Pred. No. 4.8e-78;  
Matches 238; Conservative 86; Mismatches 154; Indels 2; Gaps 2;  
Qy 6 NGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVMIPPAMKGTSDNDVGYGAYDLYD 65  
Db 3 NGVMMQYFEWHLNDGKLWKQIKEDALHLDHIGTAVMIPPAYKADQDEGYATYDLYD 62  
Qy 66 LGEPNQGTVRTKGTTRNQLQAAVTSLNKNGIQYGVGVVNMHKGAGTEIVNAVEVNR 125  
Db 63 LGEPDQGTTRTKGTGTDELKQMDLHLYHIAVYLDVNLHKGAGDTEFKFVVEVDPK 122  
Qy 126 NRQETSGEVAIEAWTKFDPGCGNNHSSFKRWYHFDGTDQDSRQLQNKIYKFRGTG 185  
Db 123 ERTKALGEPPEIQGTWTKFTPPGRGDQYSSFKWNSHFNFGTDFA-QKRGVFOIQEGK 181  
Qy 186 ADWEVDVTENGNDYLMYADVMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHKYSF 245  
Db 182 ANSEGVDSNGNDYFLCNDIDLDPVSVSELNKGWKNVSNELNLDGWRDLAKHMKDQF 241  
Qy 246 TRDWLTHVRNTTKGPMFAVAFWKNLDGAIENYLNKTSWNHVSFDPVPLHYNLYNASGG 305  
Db 242 VAQFLDAVRGERGNDYFVGEVYNGDLLEADVAIEAVGHKVNLFDPVPLHYNMFQASQEGK 301  
Qy 306 YDMRNTLNSVQKHPTHTAVTFVNDHDSQPGALESFVQGVKPKPLAYALVLTREQYPS 365  
Db 302 DYDLRDLKDTLVHEHHPDLAVTIVDNDHDTQGSLSNVEDWFKPLAYGLILLMKGYPC 361  
Qy 366 VFYGDYGIPTHGVPAKSKIDPQLQAROTFAVGTQHDYFDHDDIIGWREGNSHSPNSG 425

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Db 362 LFYGYDYGIKGEKSPHTRI-IDILLDARRKAYAGDQIEVFDHPSTIGCFIRTGDEEHNGSG 420
Qy 426 LATIMSDPGCGNKWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGSVVWVKQ 485
Db 421 LVFLMSNDEAGSKIMSLGKHKGEVWHEITGSISEBITLDEEGNGSFBFSVESRLNAVWVKK 480

RESULT 14
Q8D0T8 PRELIMINARY; PRT; 486 AA.
AC Q8D0T8;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Intracellular alpha-amylase (EC 3.2.1.1).
GN AMYA OR SMU.1590.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAI59 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR EMBL; AE014990; AAM59233.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR GlycoSIDase; Hydrolase; Complete proteome.
KW GlycoSIDase; Hydrolase; Complete proteome.
SQ SEQUENCE 486 AA; 56457 MW; EF482B92FB37C4D8 CRC64;

Query Match 47.0%; Score 1274.5; DB 16; Length 486;
Best Local Similarity 48.8%; Pred. No. 1.6e-74;
Matches 236; Conservative 73; Mismatches 170; Indels 5; Gaps 4;

Qy 5 TNGTMMQYFEWYLPNDGNHNRLRDDAANLKSQGITAVWIPPAWKGTSONDVGYGYDLY 64
Db 2 TNETMMQYFEWYLPNDGKHQHLAEDASHLKNIGISKVWMPAPKGTSGNDVGYGYDLY 61

Qy 65 DLGFEFQNGVTRTKYGRNQLQAQVTSKNGIQLVGVVMMHKGADGTEIVNAVENVNR 124
Db 62 DLGFEFQNGVTRTKYGRNQLQAQVTSKNGIQLVGVVMMHKGADGTEIVNAVENVNR 121

Qy 125 SNRQETSGBEYAEATWTFDPPGGRNNHSSFKRWYHFDGTQDQSRQLQNKIYKFRGTG 184
Db 122 SNRQETSGBEYAEATWTFDPPGGRNNHSSFKRWYHFDGTQDQSRQLQNKIYKFRGTG 181

Qy 125 SNRQETSGBEYAEATWTFDPPGGRNNHSSFKRWYHFDGTQDQSRQLQNKIYKFRGTG 184
Db 122 SNRQETSGBEYAEATWTFDPPGGRNNHSSFKRWYHFDGTQDQSRQLQNKIYKFRGTG 181

Qy 185 KAW--DWEVDVTENGNDYLYMADVDMDHPEVIELHNLNMGVWYNTNMLDGFRLDAVKHIK 242
Db 181 KAW--DWEVDVTENGNDYLYMADVDMDHPEVIELHNLNMGVWYNTNMLDGFRLDAVKHIK 240

Qy 181 KAW--DWEVDVTENGNDYLYMADVDMDHPEVIELHNLNMGVWYNTNMLDGFRLDAVKHIK 242
Db 181 KAW--DWEVDVTENGNDYLYMADVDMDHPEVIELHNLNMGVWYNTNMLDGFRLDAVKHIK 240

Qy 243 YSFTRDLWTHVRNTTCKPMFAVAFWKNDLGAENYLNKTSWNHVSFVDFPLHYNLYNASN 302
Db 241 YSFTRDLWTHVRNTTCKPMFAVAFWKNDLGAENYLNKTSWNHVSFVDFPLHYNLYNASN 300

Qy 303 SGGYDVRNLTNGSVQKQPHAVTFVNDHDSQPEALESFVQWQFKPLAYALVLTREQQ 362
Db 301 SGGYDVRNLTNGSVQKQPHAVTFVNDHDSQPEALESFVQWQFKPLAYALVLTREQQ 360

Qy 363 YPSVFGDYGVGIP-THGVPAMKSKIDPLQAROTFAFGTCHDYDHDHDIIGWREGNSSH 421
Db 361 YPSVFGDYGVGIP-THGVPAMKSKIDPLQAROTFAFGTCHDYDHDHDIIGWREGNSSH 420

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Qy 422 PNSGLATIMSDPGCGNKWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGSVV 481
Db 421 PD-GVAVIISNGEANCCKRMWGEFNRNKKVFVDYLNNTCTBEVILLDDQGWGDFPVOEASLSA 479

Qy 482 WVKQ 485
Db 480 WYMK 483

RESULT 15
Q8E0M2 PRELIMINARY; PRT; 488 AA.
AC Q8E0M2;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Alpha amylase family protein.
GN SAG0708.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Masiugnani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Vessels L.R., Madsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
DR EMBL; AE014223; AAM99595.1; -.
DR TIGR; SAG0708; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 488 AA; 56555 MW; 57249E354B2F053E CRC64;

Query Match 46.4%; Score 1259.5; DB 16; Length 488;
Best Local Similarity 47.5%; Pred. No. 1.5e-73;
Matches 229; Conservative 84; Mismatches 164; Indels 5; Gaps 4;

Qy 5 TNGTMMQYFEWYLPNDGNHNRLRDDAANLKSQGITAVWIPPAWKGTSONDVGYGYDLY 64
Db 2 TNELINQAQFEWYLPNDGNHNRLRDDAANLKSQGITAVWIPPAWKGTSONDVGYGYDLY 61

Qy 65 DLGFEFQNGVTRTKYGRNQLQAQVTSKNGIQLVGVVMMHKGADGTEIVNAVENVNR 124
Db 62 DLGFEFQNGVTRTKYGRNQLQAQVTSKNGIQLVGVVMMHKGADGTEIVNAVENVNR 121

Qy 125 SNRQETSGBEYAEATWTFDPPGGRNNHSSFKRWYHFDGTQDQSRQLQNKIYKFRGTG 184
Db 122 SNRQETSGBEYAEATWTFDPPGGRNNHSSFKRWYHFDGTQDQSRQLQNKIYKFRGTG 181

Qy 185 KAW--DWEVDVTENGNDYLYMADVDMDHPEVIELHNLNMGVWYNTNMLDGFRLDAVKHIK 242
Db 181 KAW--DWEVDVTENGNDYLYMADVDMDHPEVIELHNLNMGVWYNTNMLDGFRLDAVKHIK 240

Qy 243 YSFTRDLWTHVRNTTCKPMFAVAFWKNDLGAENYLNKTSWNHVSFVDFPLHYNLYNASN 302

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[illegible]

Search completed: October 7, 2004, 00:18:54  
Job time : 53.501 secs

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Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVWIPPAWKGTSDNDVGYGA 60  
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Db 61 YDLYDLGEFNGKQGTVRTKYGTRNQLAAVTSKNGGIQVYGDVVMNHKGGADGTEIVNAV 120  
QY 121 EVNRSNRNQTSGEYAEATWTKDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180  
Db 121 EVNRSNRNQTSGEYAEATWTKDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180  
QY 181 RGTGKAWDEVDTENGNYDLYMADVDMDHPEVHELNRNGWVYTNLTNLDGFRIDAVKH 240  
Db 181 RGTGKAWDEVDTENGNYDLYMADVDMDHPEVHELNRNGWVYTNLTNLDGFRIDAVKH 240  
QY 241 IKYSFTRDMLTHVRNTTGGKMFVAEAFKNDLGAENLYNKTSWNHNSVDFVPLHYNLYNA 300  
Db 241 IKYSFTRDMLTHVRNTTGGKMFVAEAFKNDLGAENLYNKTSWNHNSVDFVPLHYNLYNA 300  
QY 301 SNSGGYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360  
Db 301 SNSGGYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360  
QY 361 QGYPSVFYGYGIPTHGVPAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420  
Db 361 QGYPSVFYGYGIPTHGVPAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420  
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGGSVS 480  
QY 481 VVVKQ 485  
Db 481 VVVKQ 485

## RESULT 2

US-08-861-837-1  
; Sequence 1, Application US/08861837  
; Patent No. 5856164  
; GENERAL INFORMATION:  
; APPLICANT: Ottrup, Helle  
; APPLICANT: Bisgaard-Frantzen, Henrik  
; APPLICANT: Ostergaard, Peter Rahbek  
; APPLICANT: Rasmussen, Michael Dolberg  
; APPLICANT: Van Der Zee, Pia  
; TITLE OF INVENTION: Alkaline Bacillus Amylase  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5856164o No. 5856164disk of No. 5856164th America  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,837  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,803  
; FILING DATE: 01-June-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harrington, James J.  
; REGISTRATION NUMBER: 38,711  
; REFERENCE/DOCKET NUMBER: 4157.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 867-0123  
; TELEFAX: (212) 878-9655

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-861-837-1

Query Match 100.0%; Score 2714; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1.7e-229;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVWIPPAWKGTSDNDVGYGA 60  
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVWIPPAWKGTSDNDVGYGA 60  
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Db 61 YDLYDLGEFNGKQGTVRTKYGTRNQLAAVTSKNGGIQVYGDVVMNHKGGADGTEIVNAV 120  
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Db 121 EVNRSNRNQTSGEYAEATWTKDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180  
QY 181 RGTGKAWDEVDTENGNYDLYMADVDMDHPEVHELNRNGWVYTNLTNLDGFRIDAVKH 240  
Db 181 RGTGKAWDEVDTENGNYDLYMADVDMDHPEVHELNRNGWVYTNLTNLDGFRIDAVKH 240  
QY 241 IKYSFTRDMLTHVRNTTGGKMFVAEAFKNDLGAENLYNKTSWNHNSVDFVPLHYNLYNA 300  
Db 241 IKYSFTRDMLTHVRNTTGGKMFVAEAFKNDLGAENLYNKTSWNHNSVDFVPLHYNLYNA 300  
QY 301 SNSGGYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360  
Db 301 SNSGGYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360  
QY 361 QGYPSVFYGYGIPTHGVPAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420  
Db 361 QGYPSVFYGYGIPTHGVPAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420  
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGGSVS 480  
QY 481 VVVKQ 485  
Db 481 VVVKQ 485

## RESULT 3

US-08-600-908A-12  
; Sequence 12, Application US/08600908A  
; Patent No. 5989169  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Bies rd-Frantzen, Henrik  
; APPLICANT: Borchert, Torben Vedel  
; TITLE OF INVENTION: '-Amylase Mutants  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/600,908A  
FILING DATE: 13-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 4394.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-600-908A-12

Query Match 100.0%; Score 2714; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1,7e-229;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNNGTGTMQYFEMWYLPNDGNHNRRLRDAANLKSIGITAVWI.PPAWKGTSONDVGYGA 60  
DB 1 HNNGTGTMQYFEMWYLPNDGNHNRRLRDAANLKSIGITAVWI.PPAWKGTSONDVGYGA 60  
QY 61 YDLVDLGEFNQKGVTRTKYGRNQLQAAYVSLKNNGIQYGDVYNNHKGADGTEIYNAV 120  
DB 61 YDLVDLGEFNQKGVTRTKYGRNQLQAAYVSLKNNGIQYGDVYNNHKGADGTEIYNAV 120  
QY 121 EVNRSNNOETSGEYALAEATKFDPPGRGNHNSFKRWYHFDGTDWDSROLONKIYKF 180  
DB 121 EVNRSNNOETSGEYALAEATKFDPPGRGNHNSFKRWYHFDGTDWDSROLONKIYKF 180  
QY 181 RGCGKADMEVDTEENGYDYIATYADVMDHPEVTHELRNMGWYNTLNLDFRIDAIVKH 240  
DB 181 RGCGKADMEVDTEENGYDYIATYADVMDHPEVTHELRNMGWYNTLNLDFRIDAIVKH 240  
QY 241 IKYSFTDMLTHVANTTGKPMFAVAEFWKNDLGAIENTYLNKTSNNHVSFDPVPLHYNL YNA 300  
DB 241 IKYSFTDMLTHVANTTGKPMFAVAEFWKNDLGAIENTYLNKTSNNHVSFDPVPLHYNL YNA 300  
QY 301 SNSGGYDMMNIIINGSVVQKHPTHAATFVDNHDSPGBALESFYQMFKPLAVALVLTRE 360  
DB 301 SNSGGYDMMNIIINGSVVQKHPTHAATFVDNHDSPGBALESFYQMFKPLAVALVLTRE 360  
QY 361 QGYPSVFEYDYGIPHTGVPAAMSKIDPLQARQTFAYGTOHDYFDHDDIIGWTRBNSS 420  
DB 361 QGYPSVFEYDYGIPHTGVPAAMSKIDPLQARQTFAYGTOHDYFDHDDIIGWTRBNSS 420  
QY 421 HPNSGLATTINSDPGGKMMYVGNKAGQVWRDITGNRTGTVITNADGNGFSVNGGSVS 480  
DB 421 HPNSGLATTINSDPGGKMMYVGNKAGQVWRDITGNRTGTVITNADGNGFSVNGGSVS 480  
QY 481 VVWKQ 485  
DB 481 VVWKQ 485

RESULT 4  
US-08-683-838A-12  
Sequence 12, Application US/08683838A  
Patent No. 6022724  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Bisg rd-Franczen, Henrik  
APPLICANT: Borchert, Torden Vedel  
TITLE OF INVENTION: "-Amylase Mutants  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6022724dsk of No. 6022724th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York

STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/683,838A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/600,908  
FILING DATE: 13-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 4394.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-683-838A-12

Query Match 100.0%; Score 2714; DB 3; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1,7e-229;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNNGTGTMQYFEMWYLPNDGNHNRRLRDAANLKSIGITAVWI.PPAWKGTSONDVGYGA 60  
DB 1 HNNGTGTMQYFEMWYLPNDGNHNRRLRDAANLKSIGITAVWI.PPAWKGTSONDVGYGA 60  
QY 61 YDLVDLGEFNQKGVTRTKYGRNQLQAAYVSLKNNGIQYGDVYNNHKGADGTEIYNAV 120  
DB 61 YDLVDLGEFNQKGVTRTKYGRNQLQAAYVSLKNNGIQYGDVYNNHKGADGTEIYNAV 120  
QY 121 EVNRSNNOETSGEYALAEATKFDPPGRGNHNSFKRWYHFDGTDWDSROLONKIYKF 180  
DB 121 EVNRSNNOETSGEYALAEATKFDPPGRGNHNSFKRWYHFDGTDWDSROLONKIYKF 180  
QY 181 RGCGKADMEVDTEENGYDYIATYADVMDHPEVTHELRNMGWYNTLNLDFRIDAIVKH 240  
DB 181 RGCGKADMEVDTEENGYDYIATYADVMDHPEVTHELRNMGWYNTLNLDFRIDAIVKH 240  
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DB 241 IKYSFTDMLTHVANTTGKPMFAVAEFWKNDLGAIENTYLNKTSNNHVSFDPVPLHYNL YNA 300  
QY 301 SNSGGYDMMNIIINGSVVQKHPTHAATFVDNHDSPGBALESFYQMFKPLAVALVLTRE 360  
DB 301 SNSGGYDMMNIIINGSVVQKHPTHAATFVDNHDSPGBALESFYQMFKPLAVALVLTRE 360  
QY 361 QGYPSVFEYDYGIPHTGVPAAMSKIDPLQARQTFAYGTOHDYFDHDDIIGWTRBNSS 420  
DB 361 QGYPSVFEYDYGIPHTGVPAAMSKIDPLQARQTFAYGTOHDYFDHDDIIGWTRBNSS 420  
QY 421 HPNSGLATTINSDPGGKMMYVGNKAGQVWRDITGNRTGTVITNADGNGFSVNGGSVS 480  
DB 421 HPNSGLATTINSDPGGKMMYVGNKAGQVWRDITGNRTGTVITNADGNGFSVNGGSVS 480  
QY 481 VVWKQ 485  
DB 481 VVWKQ 485

RESULT 5  
US-08-600-656-1

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Sequence 1, Application US/0660055
Patent No. 6093562
GENERAL INFORMATION:
APPLICANT: Bigard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318-204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-600-656-1

Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNNGTGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAWIPPAWKGSQNDVGYGA 60
DB 1 HNNGTGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAWIPPAWKGSQNDVGYGA 60
QY 61 YDLVLDGEFNQKGVTRTKYKGTNRQLAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
DB 61 YDLVLDGEFNQKGVTRTKYKGTNRQLAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
QY 121 EVNRSNRNOETSGEYALAEAMTKFDFPGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKF 180
DB 121 EVNRSNRNOETSGEYALAEAMTKFDFPGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKF 180
QY 181 RGTGKAMDWEVDTENGNVDYLMYADVMDHPEVIEHLRNNGVWYNTNLNLDGFRIDA VKH 240
DB 181 RGTGKAMDWEVDTENGNVDYLMYADVMDHPEVIEHLRNNGVWYNTNLNLDGFRIDA VKH 240
QY 241 IKYSFTBMLTHVNTTGGKPMFAVAEFWKNDLGALENYLNKTSNMHSVFDVPLHYNL YNA 300
DB 241 IKYSFTBMLTHVNTTGGKPMFAVAEFWKNDLGALENYLNKTSNMHSVFDVPLHYNL YNA 300
QY 301 SNSGGYDMRNILNGSVVQKHPHTAAVTVDNHDQPEGALESFVQWFKPLAVALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPHTAAVTVDNHDQPEGALESFVQWFKPLAVALVLTRE 360
QY 361 QGYPSVFYGDYGGIPTHGVPAKSKIDPLLAQRTFAVGTQHDYFDHDDIIGWTRBGNSS 420
DB 361 QGYPSVFYGDYGGIPTHGVPAKSKIDPLLAQRTFAVGTQHDYFDHDDIIGWTRBGNSS 420
QY 421 HNSGLATIMSDGPGNKMVYGVKNKAGQVWRDITGNRTGVTITNADGWNFSVNGGSVS 480
```

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|||||
DB 421 HNSGLATIMSDGPGNKMVYGVKNKAGQVWRDITGNRTGVTITNADGWNFSVNGGSVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485

RESULT 6
US-09-170-670-1
Sequence 1, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bigard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276.200-US
CURRENT APPLICATION NUMBER: US/09/170,670
EARLIER FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER APPLICATION NUMBER: 60/063,306
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-170-670-1

Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNNGTGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAWIPPAWKGSQNDVGYGA 60
DB 1 HNNGTGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAWIPPAWKGSQNDVGYGA 60
QY 61 YDLVLDGEFNQKGVTRTKYKGTNRQLAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
DB 61 YDLVLDGEFNQKGVTRTKYKGTNRQLAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
QY 121 EVNRSNRNOETSGEYALAEAMTKFDFPGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKF 180
DB 121 EVNRSNRNOETSGEYALAEAMTKFDFPGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKF 180
QY 181 RGTGKAMDWEVDTENGNVDYLMYADVMDHPEVIEHLRNNGVWYNTNLNLDGFRIDA VKH 240
DB 181 RGTGKAMDWEVDTENGNVDYLMYADVMDHPEVIEHLRNNGVWYNTNLNLDGFRIDA VKH 240
QY 241 IKYSFTBMLTHVNTTGGKPMFAVAEFWKNDLGALENYLNKTSNMHSVFDVPLHYNL YNA 300
DB 241 IKYSFTBMLTHVNTTGGKPMFAVAEFWKNDLGALENYLNKTSNMHSVFDVPLHYNL YNA 300
QY 301 SNSGGYDMRNILNGSVVQKHPHTAAVTVDNHDQPEGALESFVQWFKPLAVALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPHTAAVTVDNHDQPEGALESFVQWFKPLAVALVLTRE 360
QY 361 QGYPSVFYGDYGGIPTHGVPAKSKIDPLLAQRTFAVGTQHDYFDHDDIIGWTRBGNSS 420
DB 361 QGYPSVFYGDYGGIPTHGVPAKSKIDPLLAQRTFAVGTQHDYFDHDDIIGWTRBGNSS 420
QY 421 HNSGLATIMSDGPGNKMVYGVKNKAGQVWRDITGNRTGVTITNADGWNFSVNGGSVS 480
DB 421 HNSGLATIMSDGPGNKMVYGVKNKAGQVWRDITGNRTGVTITNADGWNFSVNGGSVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485
```

```
RESULT 7
US-09-170-670-7
; Sequence 7, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-170-670-7

Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWYLPNDGNHNRLRDDAANKLSKGITAVMTPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMQYFEWYLPNDGNHNRLRDDAANKLSKGITAVMTPPAWKGTSONDVGYGA 60
Qy 61 YDLYLGEFNOKGTVRTKYGTRNQLQAQAVTSLKNGIQVYGDVVMNHKGGADGTEIYNAV 120
Db 61 YDLYLGEFNOKGTVRTKYGTRNQLQAQAVTSLKNGIQVYGDVVMNHKGGADGTEIYNAV 120
Qy 121 EVNRSNRNQETSGEYAEAWTKFDPGGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYAEAWTKFDPGGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTENGYDYLMYADVMDHDEPHVHELNRNKGWVWYTNLNLGDFRIDAVKH 240
Db 181 RGTGKAWDEVDTENGYDYLMYADVMDHDEPHVHELNRNKGWVWYTNLNLGDFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVNTTCKPMFAVAEPKNDLGAIENTLNKTSWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVNTTCKPMFAVAEPKNDLGAIENTLNKTSWNHVSFVDFPLHYNLYNA 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSVFYDYGIPTHGVPAWMSKIDPLLAQRTPAYGTOHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYDYGIPTHGVPAWMSKIDPLLAQRTPAYGTOHDYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480
Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 8
US-09-193-068-1
; Sequence 1, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-1

Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWYLPNDGNHNRLRDDAANKLSKGITAVMTPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMQYFEWYLPNDGNHNRLRDDAANKLSKGITAVMTPPAWKGTSONDVGYGA 60
Qy 61 YDLYLGEFNOKGTVRTKYGTRNQLQAQAVTSLKNGIQVYGDVVMNHKGGADGTEIYNAV 120
Db 61 YDLYLGEFNOKGTVRTKYGTRNQLQAQAVTSLKNGIQVYGDVVMNHKGGADGTEIYNAV 120
Qy 121 EVNRSNRNQETSGEYAEAWTKFDPGGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYAEAWTKFDPGGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTENGYDYLMYADVMDHDEPHVHELNRNKGWVWYTNLNLGDFRIDAVKH 240
Db 181 RGTGKAWDEVDTENGYDYLMYADVMDHDEPHVHELNRNKGWVWYTNLNLGDFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVNTTCKPMFAVAEPKNDLGAIENTLNKTSWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVNTTCKPMFAVAEPKNDLGAIENTLNKTSWNHVSFVDFPLHYNLYNA 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSVFYDYGIPTHGVPAWMSKIDPLLAQRTPAYGTOHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYDYGIPTHGVPAWMSKIDPLLAQRTPAYGTOHDYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480
Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 9
US-09-193-068-7
; Sequence 7, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjrulff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-7
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US-09-193-068-7

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Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAIVWIPPAWKGTSONDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAIVWIPPAWKGTSONDVGYGA 60

QY 61 YDLVDLGEFNGKGTVRTKYGRNQLQAAVTSLKNGGIQVYGVVNMHKGADGTEIVNAV 120
DB 61 YDLVDLGEFNGKGTVRTKYGRNQLQAAVTSLKNGGIQVYGVVNMHKGADGTEIVNAV 120

QY 121 EVNRSNRNQETSGEYAIEAWTKPDPFGRGNHNSFKRWYHFDGTDQDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQETSGEYAIEAWTKPDPFGRGNHNSFKRWYHFDGTDQDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTEGNYDYLAMYADVMDHPHPEVIELRNWGVWYTTNLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTEGNYDYLAMYADVMDHPHPEVIELRNWGVWYTTNLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNTTGGKPMFAVAEFWKNDLGAIEENYLNKTSWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNTTGGKPMFAVAEFWKNDLGAIEENYLNKTSWNHVSFVDPVPLHYNLYNA 300

QY 301 SNSGGYDMRNILNGSVVQKHPHTHAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPHTHAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE 360

QY 361 QGYPSVFYGYGIGTPHGVPAWKSKIDPLLOARQTFAYGTHDHYFDHDIIGWTRGNS 420
DB 361 QGYPSVFYGYGIGTPHGVPAWKSKIDPLLOARQTFAYGTHDHYFDHDIIGWTRGNS 420

QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

QY 481 VVWKQ 485
DB 481 VVWKQ 485

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RESULT 10

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US-09-183-412-1
; Sequence 1, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-183-412-1

```

RESULT 11

```

US-09-183-412-7
; Sequence 7, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-183-412-7

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US-09-193-068-7

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Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAIVWIPPAWKGTSONDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAIVWIPPAWKGTSONDVGYGA 60

QY 61 YDLVDLGEFNGKGTVRTKYGRNQLQAAVTSLKNGGIQVYGVVNMHKGADGTEIVNAV 120
DB 61 YDLVDLGEFNGKGTVRTKYGRNQLQAAVTSLKNGGIQVYGVVNMHKGADGTEIVNAV 120

QY 121 EVNRSNRNQETSGEYAIEAWTKPDPFGRGNHNSFKRWYHFDGTDQDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQETSGEYAIEAWTKPDPFGRGNHNSFKRWYHFDGTDQDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTEGNYDYLAMYADVMDHPHPEVIELRNWGVWYTTNLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTEGNYDYLAMYADVMDHPHPEVIELRNWGVWYTTNLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNTTGGKPMFAVAEFWKNDLGAIEENYLNKTSWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNTTGGKPMFAVAEFWKNDLGAIEENYLNKTSWNHVSFVDPVPLHYNLYNA 300

QY 301 SNSGGYDMRNILNGSVVQKHPHTHAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPHTHAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE 360

QY 361 QGYPSVFYGYGIGTPHGVPAWKSKIDPLLOARQTFAYGTHDHYFDHDIIGWTRGNS 420
DB 361 QGYPSVFYGYGIGTPHGVPAWKSKIDPLLOARQTFAYGTHDHYFDHDIIGWTRGNS 420

QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

QY 481 VVWKQ 485
DB 481 VVWKQ 485

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```

Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGKITAVWIPPAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGKITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLVLDLGEFNGKGTVRTKYGRNQLQAATVSLKNGGIQVYGVVVMNHKGGADGTEIVNAV 120
Db 61 YDLVLDLGEFNGKGTVRTKYGRNQLQAATVSLKNGGIQVYGVVVMNHKGGADGTEIVNAV 120
Qy 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNGYDYLMDVMDHPEVTHELRNMGVWYTTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDYLMDVMDHPEVTHELRNMGVWYTTNLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNTTGKPMFAVAEPKNDLGAENYLNKTSWNHVSFVDFVPLHNLNA 300
Db 241 IKYSFTRDWLTHVRNTTGKPMFAVAEPKNDLGAENYLNKTSWNHVSFVDFVPLHNLNA 300
Qy 301 SMSGYYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
Db 301 SMSGYYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
Qy 361 QGYPVSFYGYGIPTHGVPAKSKIDPLLAQRTFAYGTQHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPVSFYGYGIPTHGVPAKSKIDPLLAQRTFAYGTQHDYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 12
US-09-354-191A-1
; Sequence 1, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; STREET: No. 62970380 No. 6297038disk of No. 6297038th America, Inc.
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,191A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728

```

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; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-354-191A-1

Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGKITAVWIPPAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGKITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLVLDLGEFNGKGTVRTKYGRNQLQAATVSLKNGGIQVYGVVVMNHKGGADGTEIVNAV 120
Db 61 YDLVLDLGEFNGKGTVRTKYGRNQLQAATVSLKNGGIQVYGVVVMNHKGGADGTEIVNAV 120
Qy 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNGYDYLMDVMDHPEVTHELRNMGVWYTTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDYLMDVMDHPEVTHELRNMGVWYTTNLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNTTGKPMFAVAEPKNDLGAENYLNKTSWNHVSFVDFVPLHNLNA 300
Db 241 IKYSFTRDWLTHVRNTTGKPMFAVAEPKNDLGAENYLNKTSWNHVSFVDFVPLHNLNA 300
Qy 301 SMSGYYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
Db 301 SMSGYYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
Qy 361 QGYPVSFYGYGIPTHGVPAKSKIDPLLAQRTFAYGTQHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPVSFYGYGIPTHGVPAKSKIDPLLAQRTFAYGTQHDYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 13
US-09-291-023A-19
; Sequence 19, Application US/09291023A
; Patent No. 6309871
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borcherdt, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoesck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0

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; SEQ ID NO 19
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus
US-09-291-023A-19

Query Match      100.0%; Score 2714; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWI PPAWKGTSONDVGYGA 60
    |||
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWI PPAWKGTSONDVGYGA 60

Qy 61 YDLIDLGEFNGKQTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVMNHKGGADGTEI VNAV 120
    |||
Db 61 YDLIDLGEFNGKQTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVMNHKGGADGTEI VNAV 120

Qy 121 EVNRSNRNOETSGEYAEAWTKFDFPGRGNHSSFKWRWYHFDGTDWDSRQLQNKIYKF 180
    |||
Db 121 EVNRSNRNOETSGEYAEAWTKFDFPGRGNHSSFKWRWYHFDGTDWDSRQLQNKIYKF 180

Qy 181 RGTGKAWDEVDTENGNYDYLMAVDMDHPHPEVIELRNKGVWYTNLTNLDGFRIDAVKH 240
    |||
Db 181 RGTGKAWDEVDTENGNYDYLMAVDMDHPHPEVIELRNKGVWYTNLTNLDGFRIDAVKH 240

Qy 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFKNDLGA IENYLNKTSWNHVSFVDPVPLHYNLYNA 300
    |||
Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFKNDLGA IENYLNKTSWNHVSFVDPVPLHYNLYNA 300

Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
    |||
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420
    |||
Db 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420

Qy 421 HPNSGLATIMSDGPGGNKMYGVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
    |||
Db 421 HPNSGLATIMSDGPGGNKMYGVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VWVQK 485
    |||
Db 481 VWVQK 485

RESULT 14
US-09-290-734-1
; Sequence 1, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus sp.
US-09-290-734-1

Query Match      100.0%; Score 2714; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWI PPAWKGTSONDVGYGA 60
    |||
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWI PPAWKGTSONDVGYGA 60

Qy 61 YDLIDLGEFNGKQTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVMNHKGGADGTEI VNAV 120
    |||
Db 61 YDLIDLGEFNGKQTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVMNHKGGADGTEI VNAV 120

Qy 121 EVNRSNRNOETSGEYAEAWTKFDFPGRGNHSSFKWRWYHFDGTDWDSRQLQNKIYKF 180
    |||
Db 121 EVNRSNRNOETSGEYAEAWTKFDFPGRGNHSSFKWRWYHFDGTDWDSRQLQNKIYKF 180

Qy 181 RGTGKAWDEVDTENGNYDYLMAVDMDHPHPEVIELRNKGVWYTNLTNLDGFRIDAVKH 240
    |||
Db 181 RGTGKAWDEVDTENGNYDYLMAVDMDHPHPEVIELRNKGVWYTNLTNLDGFRIDAVKH 240

Qy 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFKNDLGA IENYLNKTSWNHVSFVDPVPLHYNLYNA 300
    |||
Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFKNDLGA IENYLNKTSWNHVSFVDPVPLHYNLYNA 300

Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
    |||
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420
    |||
Db 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420

Qy 421 HPNSGLATIMSDGPGGNKMYGVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
    |||
Db 421 HPNSGLATIMSDGPGGNKMYGVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VWVQK 485
    |||
Db 481 VWVQK 485

RESULT 15
US-09-290-734-7
; Sequence 7, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus sp.
US-09-290-734-7

Query Match      100.0%; Score 2714; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWI PPAWKGTSONDVGYGA 60
    |||
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWI PPAWKGTSONDVGYGA 60

Qy 61 YDLIDLGEFNGKQTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVMNHKGGADGTEI VNAV 120
    |||
Db 61 YDLIDLGEFNGKQTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVMNHKGGADGTEI VNAV 120
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Db	61	YDYLDELGEFNOGKTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVNHNKGGADGTEIVNAV	120
Qy	121	EVNRSNRNQETSGEYIAIEAWTKFDFPGRGNHSSFKWRWYHFDGTDWDQSRQLQNKIYKF	180
Db	121	EVNRSNRNQETSGEYIAIEAWTKFDFPGRGNHSSFKWRWYHFDGTDWDQSRQLQNKIYKF	180
Qy	181	RGTCAMDWEVDTENGNYDYLIMYADVMDHPEVTHELRNMGVWYTNLTLDGFRIDAVKH	240
Db	181	RGTCAMDWEVDTENGNYDYLIMYADVMDHPEVTHELRNMGVWYTNLTLDGFRIDAVKH	240
Qy	241	IKYSFTRDWLTHVRNTTGKPMFAVAEFWKNDLGAIENYLNKTSWNHVSFVDPVPLHYNLYNA	300
Db	241	IKYSFTRDWLTHVRNTTGKPMFAVAEFWKNDLGAIENYLNKTSWNHVSFVDPVPLHYNLYNA	300
Qy	301	SNSGGYDMRNILNGSVVQKHPHTHATFVDNHDSPGCEALSFVQOWFKPLAYALVLTRE	360
Db	301	SNSGGYDMRNILNGSVVQKHPHTHATFVDNHDSPGCEALSFVQOWFKPLAYALVLTRE	360
Qy	361	QGYPSVFGDYIGIPTHGVPAMKSKIDPQLQAROTFAYGTOHDYFDHHDIIIGWTREGNSS	420
Db	361	QGYPSVFGDYIGIPTHGVPAMKSKIDPQLQAROTFAYGTOHDYFDHHDIIIGWTREGNSS	420
Qy	421	HPNSGLATINSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGNFSVNGGSVS	480
Db	421	HPNSGLATINSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGNFSVNGGSVS	480
Qy	481	VWVKQ 485	
Db	481	VWVKQ 485	

Search completed: October 7, 2004, 00:47:05  
Job time : 17.0278 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.50628 Seconds  
(without alignments)  
2968.867 Million cell updates/sec

Title: US-09-925-576C-2

Perfect score: 2714

Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGNGNFSVNGSVVWVKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2440	89.9	518	1 AMT6_BACS7	P19571 bacillus sp
2	1905	70.2	512	1 AMY_BACLI	P06278 bacillus li
3	1892.5	69.7	549	1 AMY_BACST	P06279 bacillus li
4	1850	68.2	514	1 AMY_BACAM	P00692 bacillus am
5	1074	39.6	494	1 AMY2_SALTY	P26613 salmonella
6	1049	38.7	495	1 AMY2_ECOLI	P26612 escherichia
7	316	11.6	1196	1 AMYB_PASPO	P21543 paenibacill
8	305.5	11.3	421	1 AMYA_VIGMU	P17859 vigna mungo
9	294	10.8	440	1 AM3A_ORYSA	P27932 oryza sativ
10	289.5	10.7	551	1 AMT4_PSESA	P22963 pseudomonas
11	285	10.5	548	1 AMT4_PSEST	P13507 pseudomonas
12	270.5	10.0	435	1 AM3D_ORYSA	P27933 oryza sativ
13	269	9.9	713	1 CDGT_BACS8	P17692 bacillus sp
14	268	9.9	713	1 CDGT_BACS0	P05618 bacillus sp
15	266.5	9.8	719	1 AMYM_BACST	P19531 bacillus st
16	266	9.8	712	1 CDGT_BACS3	P09121 bacillus sp
17	265.5	9.8	427	1 AMY2_HORVU	P04063 hordeum vul
18	265	9.8	703	1 CDGT_BACS2	P31746 bacillus sp
19	261	9.6	368	1 AMY3_HORVU	P04747 hordeum vul
20	259	9.5	438	1 AM3B_ORYSA	P27937 oryza sativ
21	258.5	9.5	438	1 AMY1_HORVU	P00693 hordeum vul
22	257.5	9.5	413	1 AMY3_WHEAT	P08117 triticum ae
23	257	9.5	713	1 CDGT_BACSP	P30921 bacillus sp
24	256	9.4	429	1 AMY6_HORVU	P04750 hordeum vul
25	256	9.4	437	1 AM3C_ORYSA	P27939 oryza sativ
26	255	9.4	437	1 AM3E_ORYSA	P27934 oryza sativ
27	255	9.4	713	1 CDGU_BACCI	P43379 bacillus ci
28	254.5	9.4	428	1 AMY1_ORYSA	P17654 oryza sativ
29	248	9.1	710	1 CDGT_THETU	P26827 thermoanaer
30	247.5	9.1	718	1 CDGT_BACCI	P30920 bacillus ci
31	246.5	9.1	718	1 CDGT_BACSS	P31747 bacillus sp
32	242	8.9	528	1 AMY_BACCI	P08137 bacillus ci
33	239.5	8.8	443	1 AM2A_ORYSA	P27935 oryza sativ

## ALIGNMENTS

## RESULT 1

ID	AMT6_BACS7	STANDARD;	PRT;	518 AA.
AC	P19571;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amylase)			
OS	(Maltohexaosase-producing amylase) (Exo-maltohexaohydrolase).			
OS	Bacillus sp. (strain 707).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1416;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.			
RX	MEDLINE=88162814; PubMed=3258152;			
RA	Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;			
RT	"Nucleotide sequence of the maltohexaosase-producing amylase gene from an alkalophilic Bacillus sp. #707 and structural similarity to liquefying type alpha-amylases";			
RL	Biochem. Biophys. Res. Commun. 151:25-31 (1988).			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylaceous polysaccharides so as to remove successive maltohexaosae residues from the non-reducing chain ends.			
CC	-1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By similarity).			
CC	-1- PATHWAY: Starch degradation.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; M18862; AAA22231.1; -.			
DR	PIR; A27705; A27705.			
DR	HSSP; P06278; 1VJS.			
DR	InterPro; IPR006589; Alp amyl cat sub.			
DR	InterPro; IPR006047; Alpha_amyl_cat.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAAMYLASE.			
DR	SMART; SM00642; Amy; 1.			
KW	Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.			
FT	SIGNAL 1 33			
FT	CHAIN 34 518			
FT	ACT_SITE 269 269			
FT	ACT_SITE 273 273			
FT	ACT_SITE 366 366			
FT	ACT_SITE 139 139			
FT	METAL 196 196			
FT	METAL 219 219			
FT	GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.			
FT	BY SIMILARITY.			
FT	BY SIMILARITY.			
FT	BY SIMILARITY.			
FT	CALCIUM 1 (BY SIMILARITY).			
FT	CALCIUM 2 AND SODIUM (BY SIMILARITY).			
FT	CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).			

P14014 bacillus li  
P31797 bacillus st  
P27941 oryza sativ  
P31835 paenibacill  
Q02905 aspergillus  
Q02906 aspergillus  
P10529 aspergillus  
P21567 saccharomyc  
P04830 paenibacill  
P30292 aspergillus  
P80099 thermotoga  
O86956 thermotoga

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FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY) .
FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY) .
FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY) .
FT METAL 240 240 CALCIUM 2 (BY SIMILARITY) .
FT METAL 242 242 CALCIUM 2 (BY SIMILARITY) .
FT METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
SIMILARITY).
Query Match 89.9%; Score 2440; DB 1; Length 518;
Best Local Similarity 87.6%; Pred. No. 4.8e-159;
Matches 425; Conservative 32; Mismatches 28; Indels 0; Gaps 0;
Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLLRDDAANLKSIGITAVWIPPAWKGSQNDVGYGA 60
Db 34 HHNGTGTMMQYFEWYLPNDGNHNRLLSDASNLKSIGITAVWIPPAWKGSQNDVGYGA 93
Qy 61 YDLVDLGEFNQKGVTRKYGRNLOAAYVSLKNGIQVYGDVVNNHKGADGTEIVNAV 120
Db 94 YDLVDLGEFNQKGVTRKYGRNLOAAYVSLKNGIQVYGDVVNNHKGADGTEIVNAV 153
Qy 121 EVNRSNRNQTSGEYATEAWTKPDPGKGNHSSFKWRWYHFDGTDWDSQRLQNKIYKF 180
Db 154 EVNPNRNQEVGYETIETWTRFDPGKGNHSSFKWRWYHFDGTDWDSQRLQNKIYKF 213
Qy 181 RGTGKADWEVDTEGNYDYLMYADVDMDHPHPEVIELRNKGVWYTNLTLDGFRIDAVKH 240
Db 214 RGHGKADWEVDTEGNYDYLMYADVDMDHPHPEVIELRNKGVWYTNLTLDGFRIDAVKH 273
Qy 241 IKYSFTDMLTHVNTTCKMPFAVAEFAEKNDLGAENIYAKTSWNHVSFVDFPHLYNLNA 300
Db 274 IKYSFTDMLTHVNTTCKMPFAVAEFAEKNDLGAENIYAKTSWNHVSFVDFPHLYNLNA 333
Qy 301 SNSGGYDMRNILSGSVVQKHPHTAVTFVDNHDSPQGEALLESFVQWFKPLAYALVLTRE 360
Db 334 SKSGGNDMNIENGTVVQHPHSHAVTFVDNHDSPQGEALLESFVEWFKPLAYALVLTRE 393
Qy 361 QGYPSVFYGYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDIIGWTRGNS 420
Db 394 QGYPSVFYGYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDIIGWTRGNTA 453
Qy 421 HPNSGLATIMSDGPGKNNVYKNGKAGQWRDITGNTGTGTINADGWNFVNGGSVS 480
Db 454 HPNSGLATIMSDGPGKNNVYKNGKAGQWRDITGNTGTGTINADGWNFVNGGSVS 513
Qy 481 VWYKQ 485
Db 514 IWYK 518
RESULT 2
ID AMY_BACLI STANDARD; PRT; 512 AA.
AC P06278; Q84171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase) (BLA).
GN AMYS OR AMYL
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE=86111694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
RT amino acid sequences of three bacterial liquefying alpha-amylases
RT deduced from the DNA sequences.";
```

```
RL J. Biochem. 98:1147-1156(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=861195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Requadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX Shahhoseini M., Ziaei A.A., Ghaemi N., Pourbabaee A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RN Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Ortlepp S.A., Ollington J.P., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372(1984).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Laoide B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to
RT promoter-independent catabolite repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2435-2442(1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373(1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=2192788; PubMed=11997021;
RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
RT "Action pattern and subsite mapping of Bacillus licheniformis
RT alpha-amylase (BLA) with modified maltotriogalactaride substrates.";
RL FEBS Lett. 518:79-82(2002).
RN [8]
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RX STRAIN=ATCC 6598; PubMed=2394736;
RA Declerck N., Joyet P., Gaillardin C., Maeson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15488(1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RX STRAIN=ATCC 6598; PubMed=8771184;
RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037(1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RX ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
AND GLU-365.
RN [11]
RP STRAIN=ATCC 6598; PubMed=10966804;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057(2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RX STRAIN=ATCC 6598;
```

RX MEDLINE=22622182; PubMed=12736372;  
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,  
RA Gaillardin C.;  
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and  
RL modulation of its stability over a 50 degrees C temperature range.";  
RL Protein Eng. 16:287-293(2003).  
RN [12]  
RP MUTAGENESIS OF TRP-292 AND VAL-315.  
RC STRAIN=ATCC 27811;  
RX MEDLINE=22797417; PubMed=12915728;  
RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;  
RT "Alpha-amylase from Bacillus licheniformis mutants near to the  
RT catalytic site: effects on hydrolytic and transglycosylation  
RT activity.";  
RL Protein Eng. 16:505-514(2003).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RC STRAIN=ATCC 27811;  
RX MEDLINE=95182462; PubMed=7877175;  
RA Machius M., Wiegand G., Huber R.;  
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-  
RT amylase at 2.2-A resolution.";  
RL J. Mol. Biol. 246:545-559(1995).  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RX MEDLINE=98212915; PubMed=9551551;  
RA Machius M., Declerck N., Huber R., Wiegand G.;  
RT "Activation of Bacillus licheniformis alpha-amylase through a  
RT disorder-->order transition of the substrate-binding site mediated  
RT by a calcium-sodium-calcium metal triad.";  
RL Structure 6:281-292(1998).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.  
RX MEDLINE=20384196; PubMed=10924103;  
RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Prantzen H.,  
RA Svendsen A., Borchert T.V., Bauter Z., Wilson K.S., Davies G.J.;  
RT "Structural analysis of a chimeric bacterial alpha-amylase.  
RT High-resolution analysis of native and ligand complexes.";  
RL Biochemistry 39:9099-9107(2000).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT  
RX HL62V/N219P/A238V/Q293S/N294Y.  
RC STRAIN=ATCC 6598;  
RX MEDLINE=22538505; PubMed=12540849;  
RA Machius M., Declerck N., Huber R., Wiegand G.;  
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through  
RT introduction of hydrophobic residues at the surface.";  
RL J. Biol. Chem. 278:11546-11553(2003).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
CC linkages in oligosaccharides and polysaccharides.  
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.  
CC -1- SUBUNIT: Monomer.  
CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature  
CC liquefaction of starch-containing washes and in the detergent  
CC industry to remove starch. Sold under the name Termamyl by  
CC Novozymes.  
CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH  
CC values (up to pH 11) and at high temperatures (up to 100 degrees  
CC Celsius).  
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
CC  
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CC  
CC EMBL; X03236; CAA26981.1; --  
DR EMBL; M38570; AAA22226.1; --  
DR EMBL; M13256; AAA22240.1; --  
DR EMBL; K01984; AAA22193.1; --

DR EMBL; AF438149; AAO26743.1; --  
DR EMBL; M26412; AAA22237.1; --  
DR EMBL; A17930; CAA01355.1; --  
DR PIR; A91997; ALBSL.  
DR PDB; 1BLI; 23-MAR-99.  
DR PDB; 1BPL; 17-AUG-96.  
DR PDB; 1E3X; 21-JUN-01.  
DR PDB; 1E3Z; 24-JUN-03.  
DR PDB; 1E40; 24-JUN-03.  
DR PDB; 1E43; 21-JUN-01.  
DR PDB; 1O80; 03-APR-03.  
DR PDB; 1VJ5; 12-MAR-97.  
DR InterPro; IPR006589; Alp\_amyl\_cat\_sub.  
DR InterPro; IPR006047; Alpha\_amyl\_cat.  
DR InterPro; IPR006046; Glyco\_hydro\_13.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR PRINTS; PR00110; ALPHAAMYLASE.  
DR SMART; SM00642; Amy; 1.  
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
KW Signal; 3D-structure.  
FT SIGNAL 1 29  
FT CHAIN 30 512 ALPHA-AMYLASE.  
FT ACT\_SITE 260 260  
FT ACT\_SITE 264 264  
FT ACT\_SITE 357 357  
FT METAL 133 133  
FT METAL 190 190  
FT METAL 210 210  
FT METAL 212 212  
FT METAL 223 223  
FT METAL 229 229  
FT METAL 231 231  
FT METAL 233 233  
FT METAL 233 233  
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Best Local Similarity 68.9%; Pred. No. 1.3e-122; Indels 10; Gaps 4;  
Matches 334; Conservative 65; Mismatches 76;  
Qy 6 NGTMMQYFEWYLPNDGNHNNRLRDAANLKSIGITAVIIPPWKGTQNDVGVGAYDLYD 65  
Db 33 NGTLMQYFEWYMPNDGQHWKRLQNDASAYLAEHGITAVIIPPWKGTQNDVGVGAYDLYD 92  
Qy 66 LGFBNQKGTVRTKTYTRNLQAAVTSLNKNGIQYGVGVVNNHKGAGDTEIVNAVENRS 125  
Db 93 LGFBNQKGTVRTKTYTRNLQAAVTSLNKNGIQYGVGVVNNHKGAGDTEIVNAVENRS 152  
Qy 126 NRQNETSGEYAIKAWTKFDPFGGRNNHSSFKWYHFDGTDQSRQLQNKIKYKFGTGG 185  
Db 153 DRNRVISGEHRIKAWTHFHPFGRGSTYSDFKWHYHFDGTDQSRQLQNKIKYKFGTGG 209  
Qy 186 ADWEVDVTENGNDYLMYADVMDMDHPEVIHELNRNWGVYTTNMLDGFRIIDAVKHKYSF 245  
Db 210 ADWEVSNENGNDYLMYADVMDMDHPEVIHELNRNWGVYTTNMLDGFRIIDAVKHKYSF 269  
Qy 246 TRDWLTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHNSVDFVPLHNLNNSNGG 305  
Db 270 LRDWNVHREKTKGEMFTVAEYQNDLGAENYLNKTSWNHNSVDFVPLHNLNNSNGG 329  
Qy 306 YDMRNLINGSVYQKHPHTHATVFDVNDHSDOPGEALSFVQMKPLAYALVLTRECVPS 365  
Db 330 GYDMRKLNLNVTYVSKHPLKAVTFVNDHSDOPGEALSFVQMKPLAYALVLTRECVPS 389  
Qy 366 VFYGDYVGIPTGG-----VPAMSKIDPLQARQTAYGTQHDYFDHHDIIIGTREGNSS 420  
Db 390 VFYGDYVGIPTGG-----VPAMSKIDPLQARQTAYGTQHDYFDHHDIIIGTREGNSS 447  
Qy 421 HPNSGLATIMSDGPGGNKMYGVGNKAGQVVRDITGNRTGTVTINADGWNFSVNGGSVS 480  
Db 448 VANSGLAALITDGGGAKRMYGVGNKAGQVVRDITGNRTGTVTINADGWNFSVNGGSVS 507  
Qy 481 VVKVQ 485  
Db 508 IYVQR 512



Db 159 DRQEIISGTTQIQWITKDFPGRNTYSSFAWRWYHFDGVDWDSRKL-SRIYKFRIGK 217  
Qy 186 AWDWEVDTEGNDYLMYADVMDHPEVIHELNRWGVYNTNLMGDFRIDAVKHIFYSF 245  
Db 218 AWDWEVDTEGNDYLMYADVMDHPEVITELKSGKWKYNTNIDGFRDLDAVKHIFSF 277  
Qy 246 TROWLTHVRNTGKPMFAVAEFKNDLGAENYLNKTSWNHSDVDPVPLHYNLYNASGG 305  
Db 278 FPDWLSVRSQTGKPLFTVGEYSYDINKLHNYIMKTNGTMSLDPALHNKFTASKSGG 337  
Qy 306 YYDMRNILNGSVVOKHPTHTVFDNHDSPGEALSFVQOQFKPLAYALVLTREOQVPS 365  
Db 338 TFDNRILMTWYLMKQDTFLAVTFVDNHDTEPGALQSWDPWFPLAYAYILTRQEGYPC 397  
Qy 366 VFYGDYVYGIPTGHPVAMKSIDPLQAROTPAYCTQHDYFDHDDIIGWTREGNSHPNSG 425  
Db 398 VFYGDYVYGIPTGHPVAMKSIDPLQAROTPAYCTQHDYFDHDDIIGWTREGVTEKPGSG 457  
Qy 426 LATIMSDPGGKMYGKAKAGQVWRDITGNRTGTTINADGWNFSVNGSGSVSVWV 483  
Db 458 LAALITDPGSGKMYGKAGKAGQVWRDITGNRTGTTINADGWNFSVNGSGSVSVWV 515

## RESULT 4

AMY\_BACAM STANDARD; PRT; 514 AA.  
AC P00692;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan  
DE Glucanohydrolase).  
OS Bacillus amyloliquefaciens.  
OX Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1390;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IH;  
RX MEDLINE=83108808; PubMed=6185474;  
RA Takkinen K., Petersson R.F., Kalkkinen N., Palva I., Soederlund H.,  
RA Kaeeriaeinen L.;  
RT Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens  
RT deduced from the nucleotide sequence of the cloned gene.";  
RL J. Biol. Chem. 258:1007-1013(1983).  
RN [2]  
RP SEQUENCE OF 32-222.  
RX MEDLINE=80241725; PubMed=6156671;  
RA Chung H.S., Friedberg F.;  
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-  
RT amylase.";  
RL Biochem. J. 185:387-395(1980).  
RN [3]  
RP SEQUENCE OF 1-96 FROM N.A.  
RX MEDLINE=82051296; PubMed=6170539;  
RA Palva I., Petersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,  
RA Soederlund H., Takkinen K., Kaeeriaeinen L.;  
RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide  
RT region of the alpha-amylase gene from Bacillus amyloliquefaciens.";  
RL Gene 15:43-51(1981).  
RN [4]  
RP SEQUENCE OF 1-39 FROM N.A.  
RX MEDLINE=88137952; PubMed=2830166;  
RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;  
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by  
RT its own signal peptide from Saccharomyces cerevisiae host cells.";  
RL Gene 59:161-170(1987).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.  
RX MEDLINE=20384196; PubMed=10924103;  
RA Brzozowski A.M., Lawson D.M., Turkmenburg J.P., Biegaard-Prantzen H.,  
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;  
RT "Structural analysis of a chimeric bacterial alpha-amylase.

RT High-resolution analysis of native and ligand complexes.";  
RL Biochemistry 39:9099-9107(2000).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
CC linkages in oligosaccharides and polysaccharides.  
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.  
CC -1- SUBUNIT: Monomer.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
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CC  
CC EMBL; J01542; AAA22191.1; -;  
DR EMBL; V00092; CAA23430.1; -;  
DR EMBL; A20154; CAA01489.1; -;  
DR EMBL; M18424; AAA22192.1; -;  
DR PIR; A92389; ALBSN.  
DR PDB; 1E3X; 21-JUN-01.  
DR PDB; 1E3Z; 24-JUN-03.  
DR PDB; 1E40; 24-JUN-03.  
DR PDB; 1E43; 21-JUN-01.  
DR InterPro; IPR006589; Alp\_aml\_cat\_sub.  
DR InterPro; IPR006047; Alpha\_aml\_cat.  
DR InterPro; IPR006046; Glyco\_hydro\_13.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR PRINTS; PR00110; ALPHAAMYLASE.  
DR SMART; SM00642; Amy; 1.  
DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
KW Signal; 3D-structure.  
FT SIGNAL 1 31  
FT CHAIN 32 514 ALPHA-AMYLASE.  
FT ACT\_SITE 262 262  
FT ACT\_SITE 292 292  
FT ACT\_SITE 359 359  
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FT METAL 331 331  
FT METAL 438 438  
FT METAL 461 461  
FT CONFLICT 54 54 L -> I (IN REF. 2).  
FT CONFLICT 64 64 I -> L (IN REF. 2).  
FT CONFLICT 79 79 S -> D (IN REF. 2).  
FT CONFLICT 84 84 G -> S (IN REF. 2).  
SQ SEQUENCE 514 AA; 58403 MW; 3DE66B3F5CCDE7E CRC64;  
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Best Local Similarity 66.4%; Pred. No. 7.3e-119;  
Matches 324; Conservative 68; Mismatches 88; Indels 8; Gaps 3;  
Qy 3 NGTNGTMMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTQNDVGYGAYD 62  
Db 30 SAVNGTLMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTQNDVGYGAYD 89  
Qy 63 LYDLGEFNQKGTVTYKTRNQLQAATVSLKNGCIQYGVGVMMHKGADTEINAVEV 122  
Db 90 LYDLGEFNQKGTVTYKTRNQLQAATVSLKNGCIQYGVGVMMHKGADTEINAVEV 149  
Qy 123 NRSNRNQTSEYQIAEWTKFDPFGGRNNHSSFKRWYTHFDGTDWDSRQLQKIKYKPRG 182  
Db 150 NPANRNQTSEYQIAEWTKFDPFGGRNNHSSFKRWYTHFDGTDWDSRQLQKIKYKPRG 208

QY 183 TCGKANDWEVDTEGNYDYLADVDMDHDPVIELRNKGVWYNTNLNLDGFRIDAVKHK 242  
 Db 209 EKGAWDWEVSSNGNYDYLADVDMDHDPVIELRNKGVWYNTNLNLDGFRIDAVKHK 268  
 QY 243 YSFTDRDLTHVNTTQKMFVAEAFWQNDLGAENLNKTSWNHSDVDPVPLHYNLYNASN 302  
 Db 269 FSFLRDVQAVRAQKEMFTVAETWQNNAGLENLNKTSFNQSVFDPVPLHYNLYNASN 328  
 QY 303 SGGYDMRNILNGSVQKHPTHAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTREQ 362  
 Db 329 QGGYDMRLLDGTVSRHPEKAVFVENHDTQPGQSLSTVQWFKELAYALVLTREQ 388  
 QY 363 YPSVFGYDYGIPTHG-----VPAMKSKIDLLQARQTFAYGTOHDYDHDHDIIGWTREG 417  
 Db 389 YPQVFGDMYG--TKGTSPKIPSLKDNIEPILKARKEYAYGPQHDYDHDHDIIGWTREG 446  
 QY 418 NSSHPNSGLATIMSDPGCNKMWYGVKNKAGQVWRDITGNRTGTVTNADGWNFSVNGG 477  
 Db 447 DSSAAKSGLAALITDGPQSGKRYAGLNKAGETWYDITGNRSVTYKIGSDGWFHVDNG 506  
 QY 478 SVSVMVKQ 485  
 Db 507 SVSIYVQK 514

RESULT 5  
 AMY2\_SALTY  
 ID AMY2\_SALTY STANDARD; PRT; 494 AA.  
 AC P26613;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan  
 DE glucanohydrolase).  
 GN AMYA OR STM1963.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OK NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SJW1103;  
 RX MEDLINE=93015717; PubMed=1400215;  
 RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;  
 RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";  
 RL J. Bacteriol. 174:6644-6652(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RT LT2.";  
 RL Nature 413:852-856(2001).  
 RN [3]  
 RP SEQUENCE OF 1-6 FROM N.A.  
 RC STRAIN=SJW1103;  
 RX MEDLINE=92407478; PubMed=15274488;  
 RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;  
 RT "Subdivision of flagellar region III of the Escherichia coli and  
 RT Salmonella typhimurium chromosomes and identification of two  
 RT additional flagellar genes.";  
 RL J. Gen. Microbiol. 138:1051-1065(1992).  
 RN [4]  
 RP SEQUENCE OF 476-494 FROM N.A.  
 RX MEDLINE=93381452; PubMed=8371104;  
 RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;  
 RT "Organization of the Escherichia coli and Salmonella typhimurium  
 RT chromosomes between flagellar regions IIIa and IIib, including a

RT large non-coding region.";  
 RL J. Gen. Microbiol. 139:1401-1407(1993).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
 CC linkages in oligosaccharides and polysaccharides.  
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
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 CC -----  
 CC EMBL; L01643; AAA27110.1; -;  
 DR EMBL; AE008787; AAL20875.1; -;  
 DR EMBL; M85241; AAA27079.1; -;  
 DR EMBL; L13280; AAA71970.1; -;  
 DR PIR; B45738; B45738.  
 DR HSP; P06278; IVJ3.  
 DR StyGene; SG10011; amyA.  
 DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
 DR InterPro; IPR006047; Alpha\_amy1\_cat.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR SMART; SM00642; Amy; 1.  
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
 KW Complete proteome.  
 FT ACT\_SITE 235 235 BY SIMILARITY.  
 FT ACT\_SITE 265 265 BY SIMILARITY.  
 FT ACT\_SITE 332 332 BY SIMILARITY.  
 FT METAL 104 104 CALCIUM (BY SIMILARITY).  
 FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY  
 FT SIMILARITY).  
 FT CONFLICT 462 462 L -> S (IN REF. 1).  
 FT SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5B47C CRC64;  
 SQ  
 Query Match 39.6%; Score 1074; DB 1; Length 494;  
 Best Local Similarity 42.7%; Pred. No. 5e-66;  
 Matches 210; Conservative 80; Mismatches 184; Indels 18; Gaps 6;  
 QY 6 NGTMQYFEWYLPNDGNHNRLRDDAANKSGITAVWIPPAWKGTSON-DVGYGAYDIY 64  
 Db 3 NPTLLQYFHWYVDPGGKLMSELAERADGLDIGNWVLPACKGASGGYSGYDYDILF 62  
 QY 65 DLGEFNQKGTVTYKGYTRNQLQAATVSLKNGIQYGVDMVNMHKGADGTEIVNAVEVNR 124  
 Db 63 DLGEFDQKGTIATKYGDKRQLLTALDAKKNIAVLDDVVVNNHMKGADEKERIRVQRVNO 122  
 QY 125 SNRNQETSCEYAIETWTFDPPGRGNHSSFKRWYHFDGTDQDSRQLQNKIYKFRG-- 182  
 Db 123 DRTQIDNNIIECEWTRYTFPARAGYSNFVDFHCFSGIDHINPD-EDGIFKIVNDY 181  
 QY 183 TCGKANDWEVDTEGNYDYLADVDMDHDPVIELRNKGVWYNTNLNLDGFRIDAVKHK 242  
 Db 182 TGDGWNDDQVDDMGNFYLMGENIDFRNHAVTEEEKYWARWMEQTHCDGDFELDAVKHP 241  
 QY 243 YSFTDRDLTHVNTTQKMFVAEAFWQNDLGAENLNKTSWNHSDVDPVPLHYNLYNASN 302  
 Db 242 AMFYKEWIEHVQAVAPKPLFIVAETWWSHEVDKLTQYIDQVKGKTLMLFDAPLQMKFHEAR 301  
 QY 303 SGGYDMRNILNGSVQKHPTHAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTREQ 362  
 Db 302 QGAEDMRHIFGTILVEADPPHATVLTVANHDTPQLQALEAPVPEWFKPLAYALILRENG 361  
 QY 363 YPSVFGYDYGIPTH-----GVPAMKSKIDPLLOARQTFAYGTOHDYDHDHDI 411  
 Db 362 VPSVFPDLYGASVEDSGENGECRCVDMFVI-NQLDLILARQFAHGIIQTLFFDHPNCI 420  
 QY 412 GWTREGNSHPSGLATIMSDPGCNKMWYGVKNKAGQVWRDITGNRTGTVTINADGWN 471



QY 472 FSVNGGSVSVVW 483  
 Db 479 FFCNGGSVSVVW 490

RESULT 7  
 AMYB\_PABPO  
 ID AMYB\_PABPO STANDARD; PRT; 1196 AA.  
 AC P21543;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Beta/alpha-amylase precursor [includes: Beta-amylase (EC 3.2.1.2);  
 DE Beta/alpha-amylase (EC 3.2.1.1)].  
 OS Paenibacillus polymyxa (Bacillus polymyxa).  
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.  
 OX NCBI\_TaxID=1406;  
 RN [1]  
 RN SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=72;  
 RA MEDLINE=87165765; PubMed=2435707;  
 RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,  
 RA Tsukagoshi N., Udaoka S.;  
 RA "Cloning and nucleotide sequence of the gene coding for enzymatically  
 RT active fragments of the Bacillus polymyxa beta-amylase.";  
 RL J. Bacteriol. 169:1564-1570(1987).  
 RN [2]  
 RN SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=72;  
 RA MEDLINE=89123046; PubMed=2464578;  
 RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,  
 RA Tsukagoshi N., Udaoka S.;  
 RA "A single gene directs synthesis of a precursor protein with beta-  
 RT and alpha-amylase activities in Bacillus polymyxa.";  
 RL J. Bacteriol. 171:375-382(1989).  
 RN [3]  
 RN SEQUENCE OF 1-776 FROM N.A.  
 RC STRAIN=ATCC 8523;  
 RA MEDLINE=87231094; PubMed=2438660;  
 RA Rhodes C., Strasser J., Friedberg F.;  
 RA "Sequence of an active fragment of B. polymyxa beta amylase.";  
 RL Nucleic Acids Res. 15:3934-3934(1987).  
 RN [4]  
 RN DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.  
 RA MEDLINE=91215008; PubMed=1827035;  
 RA Uozumi N., Matsuda T., Tsukagoshi N., Udaoka S.;  
 RA "Structural and functional roles of cysteine residues of Bacillus  
 RT polymyxa beta-amylase.";  
 RL Biochemistry 30:4594-4599(1991).  
 CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO  
 CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER  
 CC SECRETION.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in  
 CC polysaccharides so as to remove successive maltose units from the  
 CC non-reducing ends of the chains.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
 CC linkages in oligosaccharides and polysaccharides.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of  
 CC glycosyl hydrolases.  
 CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of  
 CC glycosyl hydrolases.  
 CC -----  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M15817; AAA85446.1; -;  
 CC EMBL; Y00150; CAA68344.1; -;

DR PIR; A29130; A29130.  
 DR HSPP; P36924; IB9Z.  
 DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
 DR InterPro; IPR006048; Alpha\_amy1\_C.  
 DR InterPro; IPR006047; Alpha\_amy1\_cat.  
 DR InterPro; IPR005085; CBM\_25.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR InterPro; IPR001554; Glyco\_hydro\_14.  
 DR Pfam; PF00128; alpha-amylase; 1\_14.  
 DR Pfam; PF02806; alpha-amylase\_C; 1.  
 DR Pfam; PF03423; CBM\_25; 2.  
 DR Pfam; PF01373; Glyco\_hydro\_14; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR SMART; PR00750; BETAAMYLASE.  
 DR SMART; SM00642; Amy; 1.  
 DR SMART; SM00632; Amy; C; 1.  
 DR PROSITE; PS00506; BETA\_AMYLASE\_1; 1.  
 DR PROSITE; PS00679; BETA\_AMYLASE\_2; 1.  
 DR KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;  
 KW Polysaccharide degradation; Repeat.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.  
 FT DOMAIN 36 454 BETA-AMYLASE.  
 FT REPEAT 455 558  
 FT REPEAT 559 668  
 FT DOMAIN 669 1196  
 FT DISULFID 118 126  
 FT ACT\_SITE 198 198  
 FT ACT\_SITE 394 394  
 FT MUTAGEN 118 118  
 FT MUTAGEN 126 126  
 FT MUTAGEN 358 358  
 FT CONFLICT 1 1  
 FT CONFLICT 67 67  
 FT CONFLICT 100 100  
 FT CONFLICT 154 154  
 FT CONFLICT 177 177  
 FT CONFLICT 227 228  
 FT CONFLICT 330 330  
 FT CONFLICT 425 425  
 FT CONFLICT 493 493  
 FT CONFLICT 532 532  
 FT CONFLICT 559 559  
 FT CONFLICT 665 665  
 FT CONFLICT 681 681  
 FT CONFLICT 686 686  
 FT CONFLICT 725 728  
 FT CONFLICT 736 736  
 FT CONFLICT 741 741  
 FT CONFLICT 758 758  
 SQ SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;

Query Match 11.6%; Score 316; DB 1; Length 1196;  
 Best Local Similarity 23.9%; Pred. No. 6e-14;  
 Matches 124; Conservative 68; Mismatches 189; Indels 138; Gaps 25;

QY 1 HENGTTGTMMQYFEWLPNDGNHNRRLRDAANLAKSKGTAVWIPPAWKGTSQNDV-GYG 59  
 Db 766 NYGGFNNSNDQKRW-----GGDFQGIINKLDYIKRMGFTAIWTPVTKQSEYAHGKH 821  
 QY 60 AYDLYDLGFEFNQGTVRTKYGTRNQLQAATVSLKKNIGIQVYGDVVMNHKGGADGTEIVNA 119  
 Db 822 TYDFY-----AVDGHGLTMDKLQELVRKAHDKNIAVMVDVVVNHGT----- 862  
 QY 120 VEVNRSNRNQETSGEYATEAWTKFDF-PCRGNHNSF-KRWYHFDG--TDWDQSQQLQN 175  
 Db 863 -----DFQPGNGFAKPFDDKADWYHHNGDITDGDYNSNNQ- 897  
 QY 176 KIYKFRGTGKAMDWEVDTEGNYDLYMADVMDHPEVTHELRNMGVYNTNLNDGPR 235  
 Db 898 -----WKI--ENG--DVAGLDLDLHNENPATANELKNWIKWLLNETGIDGLRL 940  
 QY 236 DAVKHIKYSFTRDMLTHVRNTTGTGKPMFAVEAPFWKNDLGAIEYNLNTKTSWNHVSFVDFPLHY 295



Db 941 DTVKHVKGLKDF-DOAANT-----FTMGIEFHGDPAAYVGDY-----TRYLDAALDFPMY 991  
 QY 296 NLVNASGGYDMRNLTNGSVQKHPHTAVT---FVDNHD-----SOPGEALESF 343  
 Db 992 TIKDV--FGHQSKRKIKDRYSDDRYRDATQNGVFIDNHDVKKFLNDASGKPGANYDKW 1049  
 QY 344 VQWFKPLAYALVLT-REQVPSVFGYDYGIPHTGVPAMKSKIDPLQLARQTFAYGTQH 402  
 Db 1050 PQ-----LKAALGFTLTSRGIPFIYQGTQEGYSGGDDPA-----NRENNFNANH 1094  
 QY 403 DYFDHDDILGWTRGNSHSHNSGLATIMSDPGNGKWM-----YVGKNGAG-----Q 449  
 Db 1095 DLYQYIAKLNYR---NNHP-----ALQNGSQREKWDVDSFYSFQSKNGDEAIVFINN 1145  
 QY 450 VWRDIT---GN-----RGTVTINADGNGFNSVNGSVSV 481  
 Db 1146 SWNSQRTTIGNFNLNGTRLTNQLNSDVSQVINGNSITV 1184  
 RESULT 8  
 AMYA VIGMU STANDARD; PRT; 421 AA.  
 AC F17859;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan  
 DE glucanohydrolase).  
 GN AMY1.1.  
 OS Vigna mungo (Rice bean) (Black gram).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
 OX NCBI\_TaxID=3915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cotyledon;  
 RX MEDLINE=90332425; PubMed=2377468;  
 RA Yamauchi D., Minamikawa T.;  
 RT "Nucleotide sequence of cDNA for alpha-amylase from cotyledons of  
 RT germinating Vigna mungo seeds.";  
 RL Nucleic Acids Res. 18:4250-4250(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94120017; PubMed=8290640;  
 RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;  
 RT "Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";  
 RL Plant Physiol. 103:1459-1459(1993).  
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
 CC linkages in oligosaccharides and polysaccharides  
 CC -I- COPACTOR: Binds 3 calcium ions per subunit (By similarity).  
 CC -I- SUBUNIT: Monomer (By similarity).  
 CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
 CC  
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 CC  
 CC EMBL; X53049; CAA37217.1; -  
 CC EMBL; X73301; CAA51734.1; -  
 CC PIR; S10514; S10514.  
 CC HSP; P04063; IAVA.  
 CC InterPro; IPR006589; Alp\_aml\_cat\_sub.  
 CC InterPro; IPR006047; Alp\_aml\_cat.  
 CC InterPro; IPR006046; Glyco\_hydro\_13.  
 CC Pfam; PF00128; alpha-amylase; 1.  
 CC PRINTS; PR00110; ALPHAAMYLASE.  
 CC SMART; SM00642; Amy; 1.

KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
 KW Signal.  
 FT CHAIN 1 23 PROBABLE.  
 FT ACT\_SITE 24 421 ALPHA-AMYLASE.  
 FT ACT\_SITE 201 201 BY SIMILARITY.  
 FT ACT\_SITE 309 309 BY SIMILARITY.  
 FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).  
 FT METAL 133 130 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).  
 FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).  
 FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY  
 FT SIMILARITY).  
 FT METAL 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).  
 SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;  
 Query Match 11.3%; Score 305.5; DB 1; Length 421;  
 Best Local Similarity 25.6%; Pred. No. 9.1e-14;  
 Matches 100; Conservative 54; Mismatches 141; Indels 95; Gaps 15;  
 QY 9 MMQYFEWYLPDNGHNHRLRDDAANKLSKGITAVWIPPMKGTSONDVGYGAYDLYDLGE 68  
 Db 26 LFOGFNWESSKKGWYNSLNSIPDLANAGITHVWLPSPQSVSPE--GYLPGRLYDL- 82  
 QY 69 FNQKGTVRTKYGRNOLQAAVTSKNGGQVYGVGVVNNHKG--ADGTEIVNAVEVNRN 126  
 Db 83 -----ASKYGSKNELSLIAAFHEKGIKCLADIVINHRTAEKRGDIYCIPEGGTPD 135  
 QY 127 RNQETSGEYAIEAWTKPDPFGRGNHNSFKRWYHFGTDQDSRQLQNKIYKFRGTGKA 186  
 Db 136 SRQDWGSPFCRDDTAYS-DGTGNDS-----GEG 164  
 QY 187 WDWEVDTENGNYDLYMADVDMH--PEVHELBNWGVWYTNLTNLDGFRIDAVKHKYS 244  
 Db 165 YD-----AAPDIDLNPQVQRELSMMNLKLTGIFDGFGRFDFVKGYAPS 209  
 QY 245 FTRDLWLTHTVNTTKPMFAVAEFW-----KNDLGAENLYNKTSMNHSVF 289  
 Db 210 ISKIYMEQT-----KPDFAVGEKWDSSYQDGKPNYNQDSHRGALVNWVESAGGATAP 264  
 QY 290 DVPLHLYNLSNASSGGYDMRNILNG---SVQKHPHTAVTFVDNHDSPQGEALESF--- 343  
 Db 265 DFTTK-GILQAAVQGLWRLID-PNGKPPGMIGVKPENAVTFIDNHDGTSTQRLWPPFSD 322  
 QY 344 -VQWFKPLAYALVLTREQVPSVFGYDGY. 372  
 Db 323 KWMQ-----GYAVILT-HPGTPSIFYDHPF 346  
 RESULT 9  
 AM3A ORYSA STANDARD; PRT; 440 AA.  
 ID AM3A ORYSA  
 AC P27932;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-  
 DE glucan glucanohydrolase).  
 GN AMY1.2 OR AMY3A.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Japonica M202; TISSUE=Etioolated leaf;  
 RX MEDLINE=91329692; PubMed=1714318;  
 RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;  
 RT "Characterization of an alpha-amylase multigene cluster in rice.";  
 RL Plant Mol. Biol. 16:579-591(1991).

CC -- FUNCTION: Important for breakdown of endosperm starch during germination.

CC -- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

CC -- COFACTOR: Binds 3 calcium ions per subunit (By similarity).

CC -- SUBUNIT: Monomer.

CC -- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.

CC -- DEVELOPMENTAL STAGE: Expressed at a high level during germination in the aleurones cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level.

CC -- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC -----

DR EMBL; X56336; CAA39776.1; -.

DR PIR; S14958; S14958.

DR HSP; P04063; LAVA.

DR Gramene; P27932; ..

DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.

DR InterPro; IPR006047; Alpha\_amy1\_cat.

DR InterPro; IPR006046; Glyco\_hydro\_13.

DR Pfam; PF001128; alpha-amy1ase; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

DR SMART; SM00642; Amy; 1.

CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal; Multigene family.

CC SIGNAL 1 26

CC CHAIN 27 440

CC ACT\_SITE 207 207

CC ACT\_SITE 315 315

CC ACT\_SITE 119 119

CC METAL 145 145

CC METAL 155 155

CC METAL 166 166

CC METAL 169 169

CC METAL 170 170

CC METAL 171 171

CC METAL 174 174

CC METAL 176 176

CC SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 10.8%; Score 294; DB 1; Length 440;

Best Local Similarity 25.8%; Pred. No. 5.8e-13;

Matches 106; Conservative 55; Mismatches 152; Indels 98; Gaps 19;

QY 9 MMQYFEW-YLPDNGNHNRLRDAANLKSIGITAVIIPPAWKGTSQNDVGYGAYDYDLG 67

DB 31 LFQGFNWSKKGQWYMLKQVGDIASAGVTHVLPPTTHSVSPQ--GYMPGRLYDLN 88

QY 68 EFNQKGTVRKYTRNQLQAQVTSKNGIQVYGDVVMHKGADGTEIVNAVEVRSNR 127

DB 89 -----ASKYGTAKLSLIAFAAKIGKCVADVNVNRCADD----- 125

QY 128 NORTSGEYATKDFPGRGNHSSFKRWYHFDGTDMDQSRQLQNKIYKPGTGKAW 187

DB 126 -KDRGVYCI-----FKGGPRGC-----LDWGPSNICDDTQYSDGTHR- 165

QY 188 DWEVDTEGNYDYLMYADVMDHPVHELNRNGVWYTNLTLDGPRIDAVKHKYSFTR 247

DB 166 ----DT---GADFAAAPDIDHLPVQLSRLWRLRDLVDFGDKWLFDAKGYSAVAR 218

QY 248 DMLTHVRNTTKMPFAVAEPKNDLG-----AIENYLNKTSNHSVFDV 291

DB 219 ----TYQN--ARPSFVVAEIIW--NSLSYDGDGKPAANQDQORQELVNVWVQVGGFATAFD 272

QY 292 PLHYNLYNASNGYYDMRNILNG---SVQKHPHTHATVFDNHDSPGSALESFVQWF 348

DB 273 TTK-GILQSAVQGBELFMERD-KDGKAPGMIGWYPERKAVTFVDNHD-----GSTQRMWP 324

QY 349 KP-----LAVLVLTREQSPYFVGYGYPHGVPMKSKIDPLQARQ 394

DB 325 FPSDKVLGYAYILT-HPGVPCIFYDQVFDW-----NLKQEINALAATRK 368

RESULT 10

AMT4\_PSESA STANDARD; PRT; 551 AA.

AC P22963;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Glucan 1,4-alpha-maltotetrahydrolase precursor (EC 3.2.1.60) (G4-amy1ase) (Maltotetraose-forming amylase) (Exo-maltotetraohydrolase)

DE (Maltotetraose-forming exo-amy1ase).

GN MTA.

OS Pseudomonas saccharophila.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Comamonadaceae.

OX NCBI\_TaxID=304;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TAM 1504;

RX MEDLINE=90005970; PubMed=2676600;

RA Zhou J., Baba T., Takano T., Kobayashi S., Arai Y.;

RT "Nucleotide sequence of the maltotetrahydrolase gene from Pseudomonas saccharophila.";

RL FEBS Lett. 255:37-41(1989).

CC -- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylaceous polysaccharides so as to remove successive maltotetraose residues from the non-reducing chain ends.

CC -- COFACTOR: Binds 2 calcium ions per subunit (By similarity).

CC -- PATHWAY: Starch degradation.

CC -- SUBUNIT: Monomer (By similarity).

CC -- SUBCELLULAR LOCATION: Secreted.

CC -- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC -----

DR EMBL; X16732; CAA34708.1; -.

DR PIR; S05667; S05667.

DR HSP; P13507; 2AMG.

DR InterPro; IPR006047; Alpha\_amy1\_cat.

DR InterPro; IPR002044; CBD\_4.

DR InterPro; IPR006046; Glyco\_hydro\_13.

DR Pfam; PF00128; alpha-amy1ase; 1.

DR Pfam; PF00686; CBM 20; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

DR ProbDom; PD001568; CBD 4; 1.

CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal.

CC SIGNAL 1 21

CC CHAIN 22 551

CC ACT\_SITE 214 214

CC ACT\_SITE 240 240

CC ACT\_SITE 315 315

CC METAL 22 22

CC METAL 23 23

CC METAL 34 34

CC METAL 37 37

CC METAL 38 38

GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

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FT METAL      137      137      CALCIUM 1 (BY SIMILARITY).
FT METAL      172      172      CALCIUM 1 (BY SIMILARITY).
FT METAL      175      175      CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL      183      183      SIMILARITY).
FT METAL      218      218      CALCIUM 1 (BY SIMILARITY).
FT METAL      218      218      CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL      218      218      SIMILARITY).
FT DISULFID   161      171      BY SIMILARITY.
FT DISULFID   237      272      BY SIMILARITY.
SQ SEQUENCE   551 AA; 5989 MW; F6D67D0BB235EA35 CRC64;

Query Match      10.7%; Score 289.5; DB 1; Length 551;
Best Local Similarity 25.0%; Pred. No. 1.5e-12;
Matches 134; Conservative 64; Mismatches 170; Indels 169; Gaps 27;

QY 2 HNGTNGTMMQFEYL-----PNDGNHNRLLRDDAANKSGITAVTWIPPAWK----- 49
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
33 YHGDEILQGFHNVVREAPND--WYNILRQASTIAADGFSALWVPWRDPSSWTDG 90
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
50 GTSQNDVGYGAYDLDLGEFNGKQTVRTKYGTNRNQLQAQVTSKNGKIQVGYGVNMHKG 109
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
91 GKSGGEGYFWDH-----FNKNG-----RYGSDAQLRQAAGALGAGVKVLYDVVPH-- 138
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
110 GADGTEIVNAVEVNRNRNQTSGEYAIETKFPFGRGNHNSFKRWTHFGTGDWDQ 169
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
139 -----MNRGYPDKIEINLPAGQGFW-RNDCADPGN-----YPNDCDDGD- 175
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
170 SRQLNKIYKPRGKAWDEVDTEGNYDLYMADVDMQHPVIELRWGVMWYVNTLN 229
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
176 -----RPIG-GE-----SDLNTGHPQI-----YGMFRDELAN 201
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
230 L-----DGRFDIAVKHKIYKFTFDLWTHVNTTKPKMFAVEFQKNDLGAIE----NYL 279
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
202 LRSYGAGGRFFDFVGVAPERVDSWSDSADSS-----FCVGELWK---GPSEYPSWDWR 254
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
280 NKTSWNH-----SVFDPVLHYNLNASNGGYDMRNILNGSVQKHPTHAVTF 328
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
255 NTASWQOIKDWSRAKCPVDFALKERMQN-----GSVADWKHGLNGNPDPRMREVAVF 310
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
329 VDNRHS--ORCE-----AL-ESFVQWQFPLAYALVLTREQYPSVF-----YGD 370
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
311 VDNRHTGYSPQNGQGHWAQDLIRQ-----AYAYILT-SPGTPVYVWVSHMYDMWGYGD 364
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
371 YGIPTHGVPAKSKIDPLQAROTFAVGTQHDYFDHDIIGWTRGNSHP-----NS 424
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
365 F-----IRQLIVRTAGVRADSALSFHSYGLVATVSGSQQLTVVALNS 410
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
425 GLATIMSDPGGKWMYVYKKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 481
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
411 DLANPGVAGSGSFSEAVNASNGQVRVNRSGSG-----DGGGNDGEGGLVNV 457

RESULT 11
AMT4_PSEST
ID _AMT4_PSEST STANDARD; PRT; 548 AA.
AC P13507;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucan 1,4-alpha-maltotetrahydrolase precursor (EC 3.2.1.60) (G4-
DE amyase) (Maltotetraose-forming amylase) (Exo-maltotetrahydrolase)
DE (Maltotetraose-forming exo-amylase).
GN AMYP.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
[1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN=MO-19;
RC MEDLINE=89155431; PubMed=2646279;
RA Fujita M., Torigoe K., Nakada T., Tausaki K., Kubota M., Sakai S.,
RA Tsujisaka Y.;

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RT "Cloning and nucleotide sequence of the gene (amyP) for
RT maltotetraose-forming amylase from Pseudomonas stutzeri MO-19.";
RL J. Bacteriol. 171:1333-1339(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 286-302.
RC STRAIN=MO-19;
RX MEDLINE=97428332; PubMed=9281429;
RY Yoshioka Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.;
RT "Crystal structures of a mutant maltotetraose-forming exo-amylase
RT cocrystallized with maltopentaose.";
RL J. Mol. Biol. 271:619-628(1997).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF VARIANTS.
RC STRAIN=MO-19;
RX MEDLINE=20027472; PubMed=10556241;
RY Hasegawa K., Kubota M., Matsuura Y.;
RT "Roles of catalytic residues in alpha-amylases as evidenced by the
RT structures of the product-complexed mutants of a maltotetraose-forming
RT amylase.";
RL Protein Eng. 12:819-824(1999).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
CC in amylaceous polysaccharides so as to remove successive
CC maltotetraose residues from the non-reducing chain ends.
CC -1- COFACTOR: Binds 2 calcium ions per subunit.
CC -1- PATHWAY: Starch degradation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: THERE ARE SEVERAL ISOENZYME FORMS OF THIS PROTEIN.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; M24516; AAA25707.1; -.
DR PIR; A32803; A32803.
DR PDB; 1GCV; 28-JAN-03.
DR PDB; 1JDA; 15-OCT-97.
DR PDB; 1JDC; 15-OCT-97.
DR PDB; 1JDD; 15-OCT-97.
DR PDB; 1Q13; 24-NOV-99.
DR PDB; 1Q15; 24-NOV-99.
DR PDB; 1QPK; 17-NOV-99.
DR PDB; 2AMG; 01-APR-97.
DR InterPro; IPR006047; Alpha_amiyl_cat.
DR InterPro; IPR02044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 548
FT ACT_SITE 214 214
FT ACT_SITE 240 240
FT ACT_SITE 315 315
FT METAL 22 22
FT METAL 22 22
GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE.
CALCIUM 2.

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FT	METAL	23	CALCIUM 2 (VIA CARBONYL OXYGEN).	FT	TURN	380	381
FT	METAL	34	CALCIUM 2.	FT	STRAND	383	387
FT	METAL	37	CALCIUM 2.	FT	STRAND	393	398
FT	METAL	38	CALCIUM 2.	FT	STRAND	403	408
FT	METAL	137	CALCIUM 1.	FT	HELIX	415	417
FT	METAL	172	CALCIUM 1.	FT	TURN	418	418
FT	METAL	175	CALCIUM 1.	FT	STRAND	424	429
FT	METAL	183	CALCIUM 1.	FT	TURN	430	433
FT	METAL	218	CALCIUM 1 (VIA CARBONYL OXYGEN).	FT	STRAND	434	438
FT	DISULFID	161		SQ	SEQUENCE	548 AA;	59876 MW; 2B87217B3379158F CRC64;
FT	DISULFID	237					
FT	CONFLICT	286					
FT	TURN	28	GSIAADWKHGLNGNDPR -> ARSPTGSTPERQSRPA (IN				
FT	TURN	34	REF. 1).				
FT	TURN	35					
FT	STRAND	40					
FT	TURN	46					
FT	HELIX	48					
FT	TURN	53					
FT	HELIX	56					
FT	TURN	63					
FT	HELIX	64					
FT	TURN	70					
FT	STRAND	74					
FT	STRAND	87					
FT	TURN	90					
FT	STRAND	92					
FT	TURN	99					
FT	STRAND	108					
FT	TURN	109					
FT	STRAND	111					
FT	HELIX	113					
FT	TURN	127					
FT	STRAND	129					
FT	STRAND	138					
FT	TURN	141					
FT	TURN	152					
FT	STRAND	157					
FT	HELIX	158					
FT	STRAND	169					
FT	TURN	170					
FT	STRAND	172					
FT	TURN	179					
FT	TURN	181					
FT	STRAND	183					
FT	TURN	186					
FT	HELIX	189					
FT	STRAND	208					
FT	HELIX	216					
FT	TURN	221					
FT	STRAND	236					
FT	TURN	245					
FT	HELIX	250					
FT	STRAND	253					
FT	TURN	259					
FT	STRAND	271					
FT	TURN	274					
FT	STRAND	277					
FT	HELIX	288					
FT	STRAND	295					
FT	TURN	301					
FT	STRAND	305					
FT	TURN	307					
FT	STRAND	314					
FT	HELIX	322					
FT	STRAND	333					
FT	TURN	336					
FT	STRAND	349					
FT	TURN	353					
FT	STRAND	354					
FT	TURN	359					
FT	STRAND	363					
FT	TURN	377					

QY	2	HNGTNGTMOYFEWYL----	PNDGNHNRLRDDAANKSKGITAVITPPPAWKGTQNDVG	57
DB	33	YHGGDEILLOGFHNVVREAPND--	WYNILRQQAATIAADGFSATWIPVPRDFSSWSDG	90
QY	58	--YGAYDLVLDGEFNQKGTVRT	KYGRNQIAQAVTSIKXNGIOVYGDVVMNHRGGADGTE	115
DB	91	SKSGGEGYFWHDFKNG----	RYGSDAQLRQAASALGGAGVKVLYDVVFNH-----	138
QY	116	YNVAEVNRSNRNQETSGEYAIE	BAWTKFDPGRCNNHSSFKRWYHFDGTDWQSRQLQN	175
DB	139	-----MNRGYDPKELNLPAGQ	GFWRNDCADPGN-----YPNDCDDGD-----	175
QY	176	KYKFRGTGKAWDWEVDTE	NGYDYLMYADVMDMDHPEVIHELNRNMGVWYTNLTNL-----	230
DB	176	---RFIG-----	GD-----ADLNTGHPQV-----YGMFRDEFTNLSQYG	207
QY	231	-DGRIDAVKHIKYSFTRD	WLTHVRNTTGKMPFAVAEFWKNDLGAIE-----NYLNKTSWN	285
DB	208	AGGFREFVRYGAPERVNS	WMTDSADNS----PCUGELWK---GPSEYPNWDWRNTASMQ	260
QY	286	H-----	SVDVPLHYNLYNASNGGYDMNINLSVQKHPHTAVTFVNDHDS	334
DB	261	QIIKWSDRACKCFVDF	FALKERMON-----GSIADWKHGLNGNDPDRWRREVAVTFVNDHDT	316
QY	335	--QPGE-----	AL--ESFVQWFKPLAYALVLTREQGYPSVF-----YGDYVGIP	376
DB	317	GYSPPQNGQGHWALQDGL	IRQ-----AYAILT-SPGTPVVTWVSHMYDWGYGDF-----	365
QY	377	HGVPAAMSKIDPLQARQ	TFAYGTOHDYFDHHDIIIGWTREGNSHPNSGLATIMSDGPGG	436
DB	366	-----IRQLIQVRR--	AAGVRAD-----SALSFH--SGVSGUATVSGS	400
QY	437	NKWMYVYVGN-----	KAGQVWRDITGNRTGVTINADGWNFS-----VNGSGSVW	482
DB	401	QQTLLVVALNSDLGNPQV	-----ASGSFSEAVNASNGQVRW	437

RESULT 12

AM3D-ORISA	STANDARD;	PRT;	435 AA.
ID	AM3D-ORISA		
AC	P27933;		
DT	01-AUG-1992 (Rel. 23, Created)		
DT	01-AUG-1992 (Rel. 23, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).		
GN	AMY1.3 OR AMY3D.		
OS	Oryza sativa (Rice).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzaceae; Oryza.		
OX	NCBI_TaxID=4530;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Japonica M202; TISSUE=Etisolated leaf;		
RX	MEDLINE=91088278; PubMed=2263460;		
RA	Huang N., Koizumi N., Reinl S., Rodriguez R.L.;		
RT	"Structural organization and differential expression of rice alpha-		

Query Match 10.0%; Score 270.5; DB 1; Length 435;  
Best Local Similarity 26.0%; Pred.NO.2.3e-11;  
Matches 103; Conservative 44; Mismatches 148; Indels 101; Gaps 19;

2 HNGTGTGTMQWFEW-YLPNDGNHWNRLRDDAANLKSKITAVTWIPPAWKGSQNDVGGA 60  
::  
21 NSGOAQVLFQGFNBSWFKQGSGWNLMKGQVDDLLAKAGVTHTWLPPSHSVAPQ--GYMP 78  
:: ::

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DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM 20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KW Transferase; Glycosyltransferase; Calcium-binding; Signal.
FT SIGNAL 1 27
FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT ACT_SITE 256 256 BY SIMILARITY.
FT ACT_SITE 284 284 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT METAL 54 54 CALCIUM 1 (BY SIMILARITY).
FT METAL 55 54 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 56 56 SIMILARITY).
FT METAL 59 59 CALCIUM 1 (BY SIMILARITY).
FT METAL 60 60 CALCIUM 1 (BY SIMILARITY).
FT METAL 80 80 CALCIUM 1 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 2 (BY SIMILARITY).
FT METAL 217 217 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 226 226 SIMILARITY).
FT METAL 226 226 CALCIUM 2 (BY SIMILARITY).
FT METAL 260 260 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 260 260 SIMILARITY).
SQ SEQUENCE 713 AA; 77420 MW; 85FB616DA687B888 CRC64;

Query Match 9.9%; Score 269; DB 1; Length 713;
Best Local Similarity 22.1%; Pred. No. 5.2e-11;
Matches 114; Conservative 77; Mismatches 195; Indels 130; Gaps 23;

QY 21 GNHW-----NLRDRAANLKSQGTAVWIPPAWKG-----TSQNDVGVGAYDYLDFGEF 69
DB 78 GGBWQGLIINKD--GVLTGCVTAIWISQPVNIYSIYSGVNTVAHYGWARDFPKT 135

QY 70 NQKGTVRTKYGRNQLQAQVTSLSKNGIQYGVDMVNMHKGADGTETVNAVEVNRNRNQ 129
DB 136 N-----PAYGTTADQNLIATAAAHAKNIKVIIDFAPNHTSPASSDQ-PSFAENGRLVDNG 188

QY 130 ETSGEVAIEAWTKDFPGRGNHSSFKWRWHPFDGTDWDSQRLQNKIYKPRGTGKANDW 189
DB 189 TLLGGYTNDTQNLF-----HHNGGTDFS----- 211

QY 190 EVDTEGNGDYLMYADVDMDDHPEVIHE-----LRNWGVWYTWTLNLDGFRIDAVKHKY 243
DB 212 --TTENGIVKGL--YDLADLNHNSTSDVYLKDAIKMW-----LDLGDIDGIRMDAVKHMPF 263

QY 244 SFTRDWLTHVRNTGKPMFAVABFW--KNDLGAIEYLNKTSWNHVSFVDFVPLHYNLNA- 300
DB 264 GWQKSFMAAVNNY--KPVFTFGWFLGVNEVGP-ENHKFANESGMSLLDFRPAQKVRQVF 320

QY 301 -SNSGGYDMRNILNGSVQ-KHPTIAVTVVDNHSQPGEALESFVQWFKPLAYALVLT 358
DB 321 RDNTDNMYGLKAMLEGSAAQYQDVQVTFIDNHDMEFHASNANRKLQALAFTLILA 380

QY 359 REGQYSVFGV-DYV-----GIPTHGVPA-----MKSXIDPLQARQTFAYGTQH 402
DB 381 R---VPAIYYGTQYMSGGTDPDNRAKIPFSFTTAYQVIQKLAIPKRNPAIAYGSTQ 437

QY 403 DYFDHDDIIQWTRG-----NSHPNSGLATIMSDGPGGNKMWYVYVGNKAKGQ 449
DB 438 ERWINDVLIYERKFGSNVAVAVNRNLNAPASISGLVTSLPQGS----- 482

QY 450 VWDITGN--RTGVTVINADG-WGNFVNGSGSVSW 482
DB 483 -YNDVLGGLLNGNTLVGSGGAASNFTLAAGGTAVW 517

RESULT 14
CDGT_BACSO
ID -CDGT_BACSO
AC P05618;
```

```
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGT.
OS Bacillus sp. (strain 1011).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87308036; PubMed=2957361;
RA Kimura K., Kataoka S., Ishii Y., Takano T., Yamane K.;
RT "Nucleotide sequence of the beta-cyclodextrin glucanotransferase gene
of alkalophilic Bacillus sp. strain 1011 and similarity of its amino
acid sequence to those of alpha-amylases.";
RL J. Bacteriol. 169:4399-4402(1987).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RA Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
RT "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A
resolution.";
RL Acta Crystallogr. D 52:1136-1145(1996).
CC -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
of a 1,4-alpha-D-glucosidic bond.
CC -!- COFACTOR: Binds 2 calcium ions per subunit.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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or send an email to license@isb-sib.ch).
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EMBL; M17366; AAA22308.1; -.
DR PIR; A26678; ALBSGI.
DR PDB; 1D7F; 17-MAR-00.
DR PDB; 1D8D; 07-APR-00.
DR PDB; 1I75; 11-APR-01.
DR PDB; 1PAM; 11-JAN-97.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C_
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KW Transferase; Glycosyltransferase; Calcium-binding; Signal;
KW 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 28 165 A1.
FT DOMAIN 166 229 B.
FT DOMAIN 230 433 A2.
FT DOMAIN 434 522 C.
```

FT	DOMAIN	523	609	D.	FT	STRAND	348	349
FT	DOMAIN	610	713	E.	FT	TURN	354	355
FT	ACT SITE	256	256		FT	TURN	362	363
FT	ACT SITE	284	284		FT	HELIX	366	378
FT	ACT SITE	355	355		FT	STRAND	382	386
FT	METAL	54	54	CALCIUM 1.	FT	TURN	387	388
FT	METAL	56	56	CALCIUM 1. (VIA CARBONYL OXYGEN).	FT	HELIX	389	391
FT	METAL	59	59	CALCIUM 1.	FT	TURN	392	392
FT	METAL	60	60	CALCIUM 1.	FT	TURN	398	399
FT	METAL	80	80	CALCIUM 1.	FT	HELIX	400	402
FT	METAL	166	166	CALCIUM 2.	FT	TURN	421	421
FT	METAL	217	217	CALCIUM 2. (VIA CARBONYL OXYGEN).	FT	HELIX	422	423
FT	METAL	226	226	CALCIUM 2.	FT	TURN	424	427
FT	METAL	260	260	CALCIUM 2. (VIA CARBONYL OXYGEN).	FT	HELIX	429	433
FT	DISULFID	70	77		FT	STRAND	435	441
FT	TURN	30	31		FT	TURN	445	452
FT	TURN	33	34		FT	TURN	453	454
FT	TURN	40	41		FT	STRAND	455	462
FT	STRAND	44	46		FT	STRAND	469	471
FT	HELIX	49	51		FT	STRAND	475	475
FT	TURN	52	52		FT	STRAND	481	483
FT	HELIX	57	59		FT	TURN	486	491
FT	HELIX	63	65		FT	STRAND	496	498
FT	STRAND	66	66		FT	STRAND	500	502
FT	TURN	68	69		FT	HELIX	503	504
FT	TURN	73	74		FT	STRAND	507	509
FT	STRAND	76	76		FT	TURN	511	512
FT	HELIX	81	89		FT	STRAND	514	519
FT	TURN	90	93		FT	STRAND	527	532
FT	HELIX	94	96		FT	STRAND	535	536
FT	TURN	97	97		FT	TURN	538	539
FT	STRAND	100	103		FT	STRAND	541	547
FT	STRAND	107	109		FT	STRAND	555	558
FT	STRAND	114	116		FT	TURN	559	560
FT	TURN	117	118		FT	STRAND	561	563
FT	STRAND	119	121		FT	HELIX	565	567
FT	TURN	124	125		FT	STRAND	568	571
FT	STRAND	129	135		FT	STRAND	575	579
FT	TURN	137	139		FT	STRAND	586	593
FT	HELIX	142	154		FT	TURN	595	596
FT	TURN	155	156		FT	STRAND	599	599
FT	STRAND	158	163		FT	STRAND	603	608
FT	TURN	165	166		FT	STRAND	613	621
FT	STRAND	167	170		FT	TURN	627	628
FT	TURN	176	177		FT	STRAND	630	635
FT	TURN	179	182		FT	HELIX	638	640
FT	STRAND	184	186		FT	TURN	641	643
FT	TURN	187	188		FT	HELIX	645	647
FT	STRAND	189	192		FT	STRAND	649	649
FT	TURN	195	196		FT	STRAND	653	653
FT	TURN	198	199		FT	TURN	660	661
FT	STRAND	202	202		FT	STRAND	663	670
FT	STRAND	207	207					
FT	HELIX	213	218					
FT	STRAND	220	220					
FT	TURN	222	223					
FT	STRAND	224	227					
FT	TURN	229	230					
FT	HELIX	232	247					
FT	TURN	248	249					
FT	STRAND	252	255					
FT	TURN	256	257					
FT	HELIX	258	260					
FT	HELIX	263	276					
FT	STRAND	280	283					
FT	TURN	289	290					
FT	HELIX	294	302					
FT	STRAND	306	308					
FT	HELIX	310	320					
FT	TURN	321	322					
FT	HELIX	327	340					
FT	TURN	342	343					
FT	HELIX	344	346					

Query Match 9.9%, Score 268; DB 1; Length 713;  
Best Local Similarity 22.2%; Pred. No. 6.1e-11;  
Matches 113; Conservative 81; Mismatches 200; Indels 114; Gaps 23;

Qy	21	GNHW-----NLRDDAANLKSKGITAVWIPPAWKG-----TSQNDVGYGAYDYLGEF	69
Db	78	GGDMQGIINKIND--GYLTGNGITAIWISQVENIYSVINYGVNNTAYHGYWARDFKKT	135
Qy	70	NQKGTVRTKYTRNQLQAAVTSLNKNGIQVYGVYVMNHKGADGTEIVNAVEVNRNRNQ	129
Db	136	N-----PAYGTMQDFKNLIDTAHAHNIKVIIDFAPNHTSPASSDD-PSFAENGLYDNG	188
Qy	130	ETSCGEYAIETWKTFDFPGRGNHSSFKRWYHFGDTQDQSRQLQNKIYKFRGTGKAWDW	189
Db	189	NLLGGYTNDTQNLF-----HHYGGTDFG---TIENGIYK-----NLYDL	224
Qy	190	-EVDTEGNGVDYLMYADVDMDPHEVIHELNRWGWYTYTNLNLGDGFRIDAVKHYSFTRD	248
Db	225	ADLNHNSSVDVYLKDAIKM-----WL--DLGVGDGIRVDVAKHMPFGWQKS	268

249 WLTHVRNTTKGPMFAVAEFKNDIGATE-----NYLNKTSNMHVSFVDFPLHNLNYSN 302  
 269 FMATINNY--KPVFTGEWF--LGVNEISPEVHQFANESGMSLLDFRAQAKARQVFRDN 323  
 303 SGYYDMRNILNGSVVQ-KHPTHTAVTFVMDHSDQSGEALSFVQWFKPLAYALVLTREQ 361  
 324 TDNMVGLKAMLEGSEVDYQVNDQVTFIDNHDMERFHTSNGDRKLEQALAFLLT---SR 380  
 362 GYPSVFVGDYVGIPTGVPAMKS-----KIDPLQARQTFAYGTQHDYF 405  
 381 GVPALYYGSGYSGGNDPNRPLSFSTTTAYQVIQKLPKRSNPAIAGVSTHERW 440  
 406 DHDDIIGWRE-GNSHPNSGLATIMSDGPGNKMVYVGNKAGQV-----WRDITGN 457  
 441 INNDVIERKFGN-----NNAVVAI-----NRNMTNPASITGLVTSLRASVNDVLGG 489  
 458 --RTGVTINADG-WGNFSVNGGSVSW 482  
 490 ILNGNTLTVGAGGAASFTLAPGTAW 517

RESULT 15  
 AMYM BACST  
 ID AMYM BACST STANDARD; PRT; 719 AA.  
 AC P19531;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Maltogenic alpha-amylase precursor (EC 3.2.1.133) (Glucan 1,4-alpha-maltohydrolase).  
 GN AMYM.  
 OS Bacillus stearothermophilus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
 OX NCBI\_TaxID=1422;  
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 34-45.  
 RC STRAIN=C599;  
 RA Diderichsen B., Christiansen L.;  
 RT "Cloning of a maltogenic alpha-amylase from Bacillus stearothermophilus.";  
 RL FEMS Microbiol. Lett. 56:53-60(1988).  
 RN [2]  
 RP REVISTONS, AND X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RX MEDLINE=93315215; PubMed=10387084;  
 RA Dauter Z., Dauter M., Brzozowski A.M., Christensen S., Borchert T.V.,  
 RA Beier L., Wilson K.S., Davies G.J.;  
 RT "X-ray structure of Novamyl, the five-domain 'maltogenic' alpha-amylase from Bacillus stearothermophilus: maltose and acarbose complexes at 1.7-A resolution.";  
 RL Biochemistry 38:8385-8392(1999).  
 CC -!- FUNCTION: Converts starch into maltose.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of (1->4)-alpha-D-glucosidic linkages in polysaccharides so as to remove successive alpha-maltose residues from the non-reducing ends of the chains.  
 CC -!- COFACTOR: Binds 3 calcium ions per subunit.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- BIOTECHNOLOGY: Used in the food industry to prevent bread from staling. Sold under the name Novamyl by Novozymes.  
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; M36539; AAA22233.1; -;  
 DR PIR; S28784; S28784.  
 DR PDB; 1QHO; 31-MAY-00.  
 DR PDB; 1QHP; 31-MAY-00.  
 DR InterPro; IPR006048; Alpha\_amyl\_C.

DR InterPro; IPR006047; Alpha\_amyl\_cat.  
 DR InterPro; IPR002044; CBD 4.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR InterPro; IPR002909; IPT\_TIG.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR Pfam; PF02806; alpha-amylase; 1.  
 DR Pfam; PF00686; CBM 20; 1.  
 DR Pfam; PF01833; TIG; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR ProDom; PD001568; CBD 4; 1.  
 DR SMART; SM00632; Amy\_C; 1.  
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal; 3D-structure.  
 FT SIGNAL 1 33 MALTOGENIC ALPHA-AMYLASE.  
 FT CHAIN 34 719  
 FT ACT\_SITE 261 261  
 FT ACT\_SITE 265 265  
 FT ACT\_SITE 289 289  
 FT ACT\_SITE 362 362  
 FT METAL 54 54  
 FT METAL 56 56  
 FT METAL 59 59  
 FT METAL 60 60  
 FT METAL 81 81  
 FT METAL 83 83  
 FT METAL 109 109  
 FT METAL 110 110  
 FT METAL 112 112  
 FT METAL 134 134  
 FT METAL 135 135  
 FT METAL 164 164  
 FT METAL 217 217  
 FT METAL 231 231  
 FT METAL 265 265  
 FT CONFLICT 109 109  
 FT CONFLICT 254 256  
 FT CONFLICT 371 371  
 FT CONFLICT 379 391  
 FT SQ SEQUENCE 719 AA; 78675 MW; B40B61AD964F7D89 CRC64;  
 Query Match 9.8%; Score 266.5; DB 1; Length 719;  
 Best Local Similarity 24.0%; Pred. No. 7.8e-11;  
 Matches 139; Conservative 72; Mismatches 206; Indels 161; Gaps 32;  
 Qy 5 TNGTWMQYFEWYLPND-----GHEWNRRLRDDAANKSKGITAVWIPPAWKG----TSQ 53  
 Db 58 TNNPAKSYGLDYPTKSKWYWGDLGVROKLPYLKQLGVTTIWLSPVLNLDLTLAGT 117  
 Qy 54 NDVGAYDLYDIGEFNQKGTVRTKQTRNQLOAAVTSLSKNNGIQVYGDVVMHKGK--- 110  
 Db 118 DNTGYHGYWTRD---EKQ---IEEHFGNWTTFDTLVNDAHQNGIKIVDFVPNHSTPFA 171  
 Qy 111 -----ADGTEIVNAVEVNSNRNQETSGEVAIEAWTKEDPPGGRGNHSSPKWRYHFDG- 164  
 Db 172 NDSTFAEGGALYN-----NGTYMGNY-----FDDATKG-----YFHNGD 206  
 Qy 165 -TDWQSRLOLNKIYKF-RGTGKAWDEVDVTENGNY-DYLMYADVMDHDEVIHELNRWG 221  
 Db 207 ISNWDREYEAQWNFTDPAGFSLA---DLSQENGTTAQYLTDAVQL-----VAH----- 253  
 Qy 222 VYTTNLTNLDGFRIDAVKHISKYSFTRDWLTHTVNTTGTGKPMFAVAEFKNDIGALINL 281  
 Db 254 -----GADGLRIDAVKHNSGFSKSLADKLYQK-KDIFLVGEWYGDGPGT-ANHLEK 303  
 Qy 282 TSW-NHS---VFDVPLHNLN---ASNCGYDMDENILNGSVVQ-KHPTHTAVTFVDNHD 334  
 Db 304 VRYANNSGVNVLDFDLNLTIRNVFGFTQMTDLNNMNVQNGEYKYNKLIIFIDNHD 363  
 Qy 335 QPGEALESFVQWFKPLAYALVLTREQYGSVFYG-----DYYGIPTHG-VPAMKS 384  
 Db 364 SRFSLVNSNKANLHQAFLILT---SRGTFSIYYGTEQYMAGNDPY---NRGMMPAFDT 417





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.5516 Seconds  
(without alignments)  
2340.424 Million cell updates/sec

Title: US-09-925-576C-2

Perfect score: 2714

Sequence: 1 HHNGTNGTMMQYFEWYLPND.....ADGNGNFSVGVSVWVKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2714	100.0	485	2 AAW31499	AAW31499 Bacillus
2	2714	100.0	485	2 AAW48260	AAW48260 Bacillus
3	2714	100.0	485	2 AAY15421	AAY15421 Teramyl-
4	2714	100.0	485	2 AAY15415	AAY15415 Bacillus
5	2714	100.0	485	2 AAY25150	AAY25150 Bacillus
6	2714	100.0	485	2 AAY07391	AAY07391 Wild type
7	2714	100.0	485	2 AAY07381	AAY07381 Wild type
8	2714	100.0	485	3 AAY99602	AAY99602 Bacillus
9	2714	100.0	485	3 AAY99608	AAY99608 Bacillus
10	2714	100.0	485	5 ABB06933	ABB06933 Bacillus
11	2714	100.0	485	5 AAU12149	AAU12149 Bacillus
12	2714	100.0	485	5 AAB47850	AAB47850 Bacillus
13	2714	100.0	485	5 ABB76586	ABB76586 Teramyl-
14	2714	100.0	485	6 ABB99480	ABB99480 Amino aci
15	2712	99.9	485	2 AAW12113	AAW12113 Alpha-amy
16	2711	99.9	485	2 AAW12121	AAW12121 Alpha-amy
17	2711	99.9	485	2 AAW12099	AAW12099 Alpha-amy
18	2711	99.9	485	2 AAW12130	AAW12130 Alpha-amy
19	2711	99.9	485	2 AAW12107	AAW12107 Alpha-amy
20	2711	99.9	485	2 AAW12119	AAW12119 Alpha-amy
21	2711	99.9	485	2 AAW12102	AAW12102 Alpha-amy
22	2711	99.9	485	2 AAW12108	AAW12108 Alpha-amy
23	2711	99.9	485	2 AAW12106	AAW12106 Alpha-amy
24	2711	99.9	485	2 AAW12129	AAW12129 Alpha-amy
25	2711	99.9	485	2 AAW12118	AAW12118 Alpha-amy

26	2711	99.9	485	2 AAW12098	AAW12098 Alpha-amy
27	2711	99.9	485	2 AAW12103	AAW12103 Alpha-amy
28	2711	99.9	485	2 AAW12104	AAW12104 Alpha-amy
29	2711	99.9	485	2 AAW12105	AAW12105 Alpha-amy
30	2711	99.9	485	2 AAW12120	AAW12120 Alpha-amy
31	2711	99.9	485	2 AAW12100	AAW12100 Alpha-amy
32	2710	99.8	485	2 AAW12117	AAW12117 Alpha-amy
33	2709	99.8	485	2 AAW12122	AAW12122 Alpha-amy
34	2709	99.8	485	2 AAW12114	AAW12114 Alpha-amy
35	2709	99.8	485	2 AAW12125	AAW12125 Alpha-amy
36	2709	99.8	485	2 AAW12124	AAW12124 Alpha-amy
37	2709	99.8	485	2 AAW12123	AAW12123 Alpha-amy
38	2709	99.8	485	2 AAW12126	AAW12126 Alpha-amy
39	2709	99.8	485	2 AAW12131	AAW12131 Alpha-amy
40	2709	99.8	485	2 AAW12127	AAW12127 Alpha-amy
41	2709	99.8	485	2 AAW12128	AAW12128 Alpha-amy
42	2708	99.8	485	2 AAW12101	AAW12101 Alpha-amy
43	2708	99.8	485	2 AAW12112	AAW12112 Alpha-amy
44	2708	99.8	485	2 AAW12111	AAW12111 Alpha-amy
45	2707	99.7	485	2 AAW12144	AAW12144 Alpha-amy

#### ALIGNMENTS

##### RESULT 1

AAW31499  
ID AAW31499 standard; protein; 485 AA.

XX AC AAW31499;

XX DT 08-APR-1998 (first entry)

XX DE Bacillus sp. alpha amylase.

XX KW Alpha amylase; hard surface cleaning; dishwashing; laundry.

XX OS Bacillus sp.

XX PN W09732961-A2.

XX PD 12-SEP-1997.

XX PF 04-MAR-1997; 97WO-US003635.

XX PR 07-MAR-1996; 96WO-US003276.

XX PA (PROC ) PROCTER & GAMBLE CO.

XX PI Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;  
Ward G;

XX DR WPI; 1997-457524/42.

XX PT Detergent compositions for hard surface cleaning and laundry use -  
contains Bacillus derived alpha amylase with improved thermostability;  
reduced calcium ion dependency etc.

XX PS Claim 1; Page 86-87; 97pp; English.

XX CC The present sequence is a Bacillus sp. alpha amylase with a specific  
activity at least 25% higher than that of Teramyl (RTM) at 25 to 55  
degrees C at pH 8 to 10, measured by the Phadebas (RTM) activity test. It  
is of use in hard surface cleaning, hand or machine dishwashing and  
laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain  
removal and fabric care are obtained by using it at a concentration of  
0.00018 to 0.06%

XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1.1e-206;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSGKITAVWIPPAWKGTSONDVGYGA 60  
 |||||  
 Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSGKITAVWIPPAWKGTSONDVGYGA 60  
 |||||  
 QY 61 YDLYDLGEFNGKGTVRTKYGTNRNQLQAAVTSLNKNGIQVYGVVNMHKGADGTEIYNVAV 120  
 |||||  
 Db 61 YDLYDLGEFNGKGTVRTKYGTNRNQLQAAVTSLNKNGIQVYGVVNMHKGADGTEIYNVAV 120  
 |||||  
 QY 121 EVNRSNRNQTSGEYAIEAWTKFDPGGRGNHSSFKRWYHFDGTDQDQSRQLQNKIYKF 180  
 |||||  
 Db 121 EVNRSNRNQTSGEYAIEAWTKFDPGGRGNHSSFKRWYHFDGTDQDQSRQLQNKIYKF 180  
 |||||  
 QY 181 RGTGKAWDEVDTENGNYDLYMADVMDHPEVIHELNRWGVWYTTNLDGFRIDAVKH 240  
 |||||  
 Db 181 RGTGKAWDEVDTENGNYDLYMADVMDHPEVIHELNRWGVWYTTNLDGFRIDAVKH 240  
 |||||  
 QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAFKNDLGAENYLNKTSWNHSHVFDVPLHYNLYNA 300  
 |||||  
 Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFKNDLGAENYLNKTSWNHSHVFDVPLHYNLYNA 300  
 |||||  
 QY 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360  
 |||||  
 Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360  
 |||||  
 QY 361 QGYPSVFYGYGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420  
 |||||  
 Db 361 QGYPSVFYGYGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420  
 |||||  
 QY 421 HPNSGLATIMSDPGGNKMYGKNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480  
 |||||  
 Db 421 HPNSGLATIMSDPGGNKMYGKNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480  
 |||||  
 QY 481 VWVKQ 485  
 |||||  
 Db 481 VWVKQ 485  
 |||||

RESULT 2

AAW48260  
 ID AAW48260 standard; protein; 485 AA.  
 XX  
 AC AAW48260;  
 XX  
 DT 02-JUL-1998 (first entry)  
 XX  
 DE Bacillus sp. alpha amylase protein #1.  
 XX  
 KW Alpha amylase; stain digestion; detergent; fabric laundry performance.  
 XX  
 OS Bacillus sp.  
 XX  
 PN WO9805748-A1.  
 XX  
 -PD 12-FEB-1998.  
 XX  
 PF 01-AUG-1996; 96WO-US012612.  
 XX  
 PR 01-AUG-1996; 96WO-US012612.  
 XX  
 XX (PROC ) PROCTER & GAMBLE CO.  
 XX  
 XX Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;  
 XX  
 XX WPI; 1998-159168/14.  
 DR  
 XX Use of specific alpha-amylase enzymes - in laundry detergent compositions  
 XX to provide effective cleaning and whitening of dingy fabrics.  
 PT  
 XX Claim 1; Page 69-70; 82pp; English.  
 PS  
 XX This sequence represents an alpha amylase from Bacillus sp. which is used  
 CC in a laundry detergent. The detergent compositions can be used for  
 CC

CC boosting fabric laundry performance or for dingy fabric cleanup

XX Sequence 485 AA;

QY Query Match 100.0%; Score 2714; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 1.1e-206; Indels 0; Gaps 0;

Matches 485; Conservative 0; Mismatches 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSGKITAVWIPPAWKGTSONDVGYGA 60

Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSGKITAVWIPPAWKGTSONDVGYGA 60

QY 61 YDLYDLGEFNGKGTVRTKYGTNRNQLQAAVTSLNKNGIQVYGVVNMHKGADGTEIYNVAV 120

Db 61 YDLYDLGEFNGKGTVRTKYGTNRNQLQAAVTSLNKNGIQVYGVVNMHKGADGTEIYNVAV 120

QY 121 EVNRSNRNQTSGEYAIEAWTKFDPGGRGNHSSFKRWYHFDGTDQDQSRQLQNKIYKF 180

Db 121 EVNRSNRNQTSGEYAIEAWTKFDPGGRGNHSSFKRWYHFDGTDQDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTENGNYDLYMADVMDHPEVIHELNRWGVWYTTNLDGFRIDAVKH 240

Db 181 RGTGKAWDEVDTENGNYDLYMADVMDHPEVIHELNRWGVWYTTNLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAFKNDLGAENYLNKTSWNHSHVFDVPLHYNLYNA 300

Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFKNDLGAENYLNKTSWNHSHVFDVPLHYNLYNA 300

QY 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360

Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360

QY 361 QGYPSVFYGYGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420

Db 361 QGYPSVFYGYGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420

QY 421 HPNSGLATIMSDPGGNKMYGKNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480

Db 421 HPNSGLATIMSDPGGNKMYGKNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480

QY 481 VWVKQ 485

Db 481 VWVKQ 485

RESULT 3

AAV15421

ID AAV15421 standard; protein; 485 AA.

XX AAV15421;

XX 22-JUL-1999 (first entry)

DE Termamyl-like alpha-amylase protein.

XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;

KW sweetener; ethanol; starch; textile desizing; starch liquefaction;

KW saccharification process.

XX Bacillus sp.

XX WO9923211-A1.

XX 14-MAY-1999.

XX 30-OCT-1998; 98WO-DK000471.

XX 30-OCT-1997; 97DK-00001240.

XX 14-JUL-1998; 98DK-00000936.

XX (NOVO ) NOVO-NORDISK AS.

XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;

```

PI Kjaerulff S;
XX
DR WPI; 1999-326987/27.
XX
XX New Termamyl-like alpha-amylase variants.
XX
XX Claim 38; Page 88-89; 115pp; English.
XX
CC The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, K107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, M457, K458, P459, G460, T461, T462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention
XX
XX Sequence 485 AA;
XX
Query Match 100.0%; Score 2714; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.1e-206;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSGITAVMIPPAWKGTQNDVGGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSGITAVMIPPAWKGTQNDVGGA 60
QY 61 YDLYDLGFEFNKQGTVRTKYGTRNQLQAATVSLKNGIQVYGDVVMNHKGGADGTEIVNAV 120
DB 61 YDLYDLGFEFNKQGTVRTKYGTRNQLQAATVSLKNGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYALEAWTKFDFPGRGNHNSFKWRWYHFDGTDWQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYALEAWTKFDFPGRGNHNSFKWRWYHFDGTDWQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTENGNYDYLMTADVMDHPEVIHELNRNMGVWYTNLTLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTENGNYDYLMTADVMDHPEVIHELNRNMGVWYTNLTLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGKPMFAVEFKNDLGAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVEFKNDLGAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
QY 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMSKIDPLQARQTFAYGQTHDYFDHHDIIIGWTREGNSS 420
DB 361 QGYPSVFYGDYGIPTHGVPAMSKIDPLQARQTFAYGQTHDYFDHHDIIIGWTREGNSS 420
QY 421 HPNSGLATIMSDPGGNKMWYGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDPGGNKMWYGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 VVYKQ 485
DB 481 VVYKQ 485

RESULT 4
ID AAY15415
XX AAY15415 standard; protein; 485 AA.
XX
AC AAY15415;
XX
DT 22-JUL-1999 (first entry)
XX

```

```

DE Bacillus strain NCIB 12512 alpha-amylase protein.
XX
XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
XX sweetener; ethanol; starch; textile desizing; starch liquefaction;
XX saccharification process.
XX
OS Bacillus sp.
XX
XX WO9923211-A1.
XX
XX 14-MAY-1999.
XX
XX 30-OCT-1998; 98WO-DK000471.
XX
XX 30-OCT-1997; 97DK-00001240.
XX
XX 14-JUL-1998; 98DK-00000936.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
XX Kjaerulff S;
XX
XX WPI; 1999-326987/27.
XX
XX New Termamyl-like alpha-amylase variants.
XX
XX Claim 38; Page 77-79; 115pp; English.
XX
CC The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, K107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, M457, K458, P459, G460, T461, T462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention
XX
XX Sequence 485 AA;
XX
Query Match 100.0%; Score 2714; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.1e-206;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSGITAVMIPPAWKGTQNDVGGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSGITAVMIPPAWKGTQNDVGGA 60
QY 61 YDLYDLGFEFNKQGTVRTKYGTRNQLQAATVSLKNGIQVYGDVVMNHKGGADGTEIVNAV 120
DB 61 YDLYDLGFEFNKQGTVRTKYGTRNQLQAATVSLKNGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYALEAWTKFDFPGRGNHNSFKWRWYHFDGTDWQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYALEAWTKFDFPGRGNHNSFKWRWYHFDGTDWQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTENGNYDYLMTADVMDHPEVIHELNRNMGVWYTNLTLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTENGNYDYLMTADVMDHPEVIHELNRNMGVWYTNLTLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGKPMFAVEFKNDLGAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVEFKNDLGAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
QY 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMSKIDPLQARQTFAYGQTHDYFDHHDIIIGWTREGNSS 420

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Db 361 QGYPSVFGDYGIPTHGVPAMKSKIDPLQARQTFAVWIPPAWKTSQNDVGYGA 480  
 QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSVS 480  
 Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSVS 480  
 QY 481 VVVKQ 485  
 Db 481 VVVKQ 485  
 RESULT 5  
 ID AAY25150 standard; protein; 485 AA.  
 AC AAY25150;  
 XX 27-AUG-1999 (first entry)  
 DT Bacillus sp. alpha-amylase protein fragment 1.  
 DE Alpha-amylase; cleaning composition; protease variant; spot removal;  
 KW detergent composition; hard surface cleaning; fabric cleaning;  
 KW dishwashing composition; oral cleaning composition; personal cleansing;  
 KW stain removal; soil removal; whiteness maintenance; dingy cleanup;  
 KW film removal.  
 XX  
 OS Bacillus sp.  
 XX WO9920723-A2.  
 XX 29-APR-1999.  
 XX 23-OCT-1998; 98WO-US022486.  
 XX 23-OCT-1997; 97US-00956323.  
 PR 23-OCT-1997; 97US-00956324.  
 PR 23-OCT-1997; 97US-00956564.  
 XX (PROC ) PROCTER & GAMBLE CO.  
 PA Ghosh CK, Baack AC, Ohtani R, Busch A, Showell MS;  
 XX WPI; 1999-404706/34.  
 XX Cleaning compositions used in e.g. detergent for cleaning hard surfaces  
 PT or fabrics, dishwashing or oral cleaning comprises protease and amylase  
 PT variants having amino acid residues.  
 XX Claim 1b(ii); Page 164-165; 169pp; English.  
 XX This invention describes novel cleaning compositions which contain a  
 CC protease variant with an amino acid substitution corresponding to  
 CC position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant.  
 CC The compositions can be used in e.g. detergent compositions, for cleaning  
 CC hard surfaces or fabrics, dishwashing compositions, oral cleaning  
 CC compositions, detergent cleaning compositions and personal cleansing  
 CC compositions. The combination of protease variants and alpha-amylase  
 CC variants in cleaning compositions can provide improved and enhanced  
 CC cleaning ability, including stain and/or soil removal and/or reduction  
 CC and/or whiteness maintenance and/or dingy cleanup and/or spot and/or film  
 CC removal and/or reduction, over conventional enzyme-containing cleaning  
 CC compositions  
 XX Sequence 485 AA;  
 SQ  
 Query Match 100.0%; Score 2714; DB 2; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHNGTNGTMQYFEWYLPNDGNHNRDLRDAANKSKGITAVWIPPAWKTSQNDVGYGA 60  
 |||||

Db 1 HHNGTNGTMQYFEWYLPNDGNHNRDLRDAANKSKGITAVWIPPAWKTSQNDVGYGA 60  
 QY 61 YLDYDLGEFNQKGTVTKYKTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120  
 |||||  
 Db 61 YLDYDLGEFNQKGTVTKYKTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120  
 |||||  
 QY 121 EVNRSNRNQETSGEYAIEAWTKFDFPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
 Db 121 EVNRSNRNQETSGEYAIEAWTKFDFPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
 |||||  
 QY 181 RGTGKAWDEVDTEGNGYDLYMAYADVMDHPPEVIHELNRWGVWYTTNLNDGFRIDAVKH 240  
 Db 181 RGTGKAWDEVDTEGNGYDLYMAYADVMDHPPEVIHELNRWGVWYTTNLNDGFRIDAVKH 240  
 |||||  
 QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFKNDLGAENYLNKTSWNHSVFDVPLHYNLYNA 300  
 Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFKNDLGAENYLNKTSWNHSVFDVPLHYNLYNA 300  
 |||||  
 QY 301 SNSGGYYDMRNILNGSVQKHPHVAFTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360  
 Db 301 SNSGGYYDMRNILNGSVQKHPHVAFTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360  
 |||||  
 QY 361 QGYPSVFGDYGIPTHGVPAMKSKIDPLQARQTFAVWIPPAWKTSQNDVGYGA 420  
 Db 361 QGYPSVFGDYGIPTHGVPAMKSKIDPLQARQTFAVWIPPAWKTSQNDVGYGA 420  
 |||||  
 QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSVS 480  
 Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSVS 480  
 |||||  
 QY 481 VVVKQ 485  
 Db 481 VVVKQ 485  
 RESULT 6  
 ID AAY07391 standard; protein; 485 AA.  
 AC AAY07391;  
 XX 16-JUL-1999 (first entry)  
 DT Wild type Termamyl(RTM)-like alpha-amylase protein #7.  
 DE Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;  
 KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;  
 KW ethanol.  
 XX Bacillus sp.  
 OS WO9919467-A1.  
 PN 22-APR-1999.  
 PD 13-OCT-1998; 98WO-DK000444.  
 PF 13-OCT-1997; 97DK-00001172.  
 PR (NOVO ) NOVO-NORDISK AS.  
 XX Svendsen A, Borchert TV, Bisgard-Frantzen H;  
 PI WPI; 1999-277632/23.  
 DR Variant alpha-amylases - useful as detergents or for textile desizing or  
 PT starch liquefaction.  
 PT Disclosure; Page 72-74; 93pp; English.  
 PS This sequence represents the parent sequence for new variants of a parent  
 CC Termamyl-like alpha-amylase with alpha-amylase activity. The variants  
 CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase

CC from either of two *Bacillus* species in W09526397, *B. stearothermophilus*,  
 CC *B. licheniformis*, *B. amyloliquefaciens* or *Bacillus* sp. #707. The alpha-  
 CC amylase variants are detergent additives for use in detergents for  
 CC dishwashing, manual or automatic laundry. The variants can also be used  
 CC for textile desizing or starch liquefaction (e.g. for production of  
 CC sweeteners or ethanol)  
 XX  
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 2; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGTSONDVGGA 60  
 Db 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGTSONDVGGA 60  
 Qy 61 YDYLDELGEFNQKGTVRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
 Db 61 YDYLDELGEFNQKGTVRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
 Qy 121 EVNRSNRNQETSGEYATEAWTKPDPGGRGNHNSFKWRWHFDGTDMDQSRQLQNKLYKF 180  
 Db 121 EVNRSNRNQETSGEYATEAWTKPDPGGRGNHNSFKWRWHFDGTDMDQSRQLQNKLYKF 180  
 Qy 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVHELNRNMGVWYTNLTLDGFRIDAVKH 240  
 Db 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVHELNRNMGVWYTNLTLDGFRIDAVKH 240  
 Qy 241 IKYSFTRDMLTHVRNTTCKPMFAVAEFWKNLDGAIENYLNKTSWNHNSVDFVPLHYNLYNA 300  
 Db 241 IKYSFTRDMLTHVRNTTCKPMFAVAEFWKNLDGAIENYLNKTSWNHNSVDFVPLHYNLYNA 300  
 Qy 301 SNSGGYVDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360  
 Db 301 SNSGGYVDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360  
 Qy 361 QGYPVSFYGDYGYGIPTHGVPAWMSKIDPLQARQTFAYGTOHDYFDHDDIIGWTREGNSS 420  
 Db 361 QGYPVSFYGDYGYGIPTHGVPAWMSKIDPLQARQTFAYGTOHDYFDHDDIIGWTREGNSS 420  
 Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWGNFVNGGSVS 480  
 Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWGNFVNGGSVS 480  
 Qy 481 VVWVKQ 485  
 Db 481 VVWVKQ 485

## RESULT 7

AA07381  
 ID AA07381 standard; protein; 485 AA.  
 XX AC  
 XX AA07381;  
 XX  
 DT 16-JUL-1999 (first entry)  
 XX  
 DE Wild type Termamyl (RTM)-like alpha-amylase protein #1.  
 XX  
 KW Variant; Termamyl; alpha-amylase; mutation; *Bacillus*; detergent;  
 KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;  
 KW ethanol.  
 XX  
 OS *Bacillus* sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 181..184  
 FT /note= "optionally 1, 2, 3 or all residues are deleted"  
 FT Misc-difference 195  
 FT /note= "optionally altered to any amino acid except an  
 FT Asn residue"  
 FT Misc-difference 206

FT /note= "optionally altered to any amino acid except a Val  
 residue"  
 FT Misc-difference 212  
 FT /note= "optionally altered to any amino acid except a Glu  
 residue"  
 FT Misc-difference 216  
 FT /note= "optionally altered to any amino acid except a Glu  
 residue"  
 FT Misc-difference 269  
 FT /note= "optionally altered to any amino acid except a Lys  
 residue"  
 XX  
 XX

W09919467-A1.

22-APR-1999.

13-OCT-1998; 98WO-DK000444.

13-OCT-1997; 97DK-00001172.

(NOVO ) NOVO-NORDISK AS.

Svendsen A, Borchert TV, Bisgard-Frantzen H;

WPI; 1999-277632/23.

Variant alpha-amylases - useful as detergents or for textile desizing or  
 starch liquefaction.

Claim 1; Page 61-63; 93pp; English.

This sequence represents the parent sequence for new variants of a parent  
 Termamyl-like alpha-amylase with alpha-amylase activity. The variants  
 comprise mutations in 2-6 regions/positions relative to an alpha-amylase  
 from either of two *Bacillus* species in W09526397, *B. stearothermophilus*,  
*B. licheniformis*, *B. amyloliquefaciens* or *Bacillus* sp. #707. The alpha-  
 amylase variants are detergent additives for use in detergents for  
 dishwashing, manual or automatic laundry. The variants can also be used  
 for textile desizing or starch liquefaction (e.g. for production of  
 sweeteners or ethanol)

SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 2; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGTSONDVGGA 60  
 Db 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGTSONDVGGA 60  
 Qy 61 YDYLDELGEFNQKGTVRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
 Db 61 YDYLDELGEFNQKGTVRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
 Qy 121 EVNRSNRNQETSGEYATEAWTKPDPGGRGNHNSFKWRWHFDGTDMDQSRQLQNKLYKF 180  
 Db 121 EVNRSNRNQETSGEYATEAWTKPDPGGRGNHNSFKWRWHFDGTDMDQSRQLQNKLYKF 180  
 Qy 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVHELNRNMGVWYTNLTLDGFRIDAVKH 240  
 Db 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVHELNRNMGVWYTNLTLDGFRIDAVKH 240  
 Qy 241 IKYSFTRDMLTHVRNTTCKPMFAVAEFWKNLDGAIENYLNKTSWNHNSVDFVPLHYNLYNA 300  
 Db 241 IKYSFTRDMLTHVRNTTCKPMFAVAEFWKNLDGAIENYLNKTSWNHNSVDFVPLHYNLYNA 300  
 Qy 301 SNSGGYVDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360  
 Db 301 SNSGGYVDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360  
 Qy 361 QGYPVSFYGDYGYGIPTHGVPAWMSKIDPLQARQTFAYGTOHDYFDHDDIIGWTREGNSS 420

Db	361	QGYPSVFYGDYIGIPTHGVPAKSKIDPLIQAQRTFAYGTQHDYFDHDDIIGHTREGNSS	420	Db	61	YDLYDLGEFNGKQGTVRTKYGTRNLQAQAVTSLKNNGLQVYGDVVMNHKGGADGTEIVNAV	120
Qy	421	HPNSGLATIMSDGPGGNKMYGKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480	Qy	121	EVNRSNRNQBTSGEYAI EAWTKFDFPGRGNHSSFKWRWYHFDGTQDWDQSRQLQNKIYKF	180
Db	421	HPNSGLATIMSDGPGGNKMYGKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480	Db	121	EVNRSNRNQBTSGEYAI EAWTKFDFPGRGNHSSFKWRWYHFDGTQDWDQSRQLQNKIYKF	180
Qy	481	VWVKQ 485		Qy	181	RGTKAWDEVDTPENGNYDYLMTYADVMDHPHPEVHEL RNKGWVWYTNLTLDGFRIDAVKH	240
Db	481	VWVKQ 485		Db	181	RGTKAWDEVDTPENGNYDYLMTYADVMDHPHPEVHEL RNKGWVWYTNLTLDGFRIDAVKH	240
RESULT 8							
AAAY99602				Qy	241	IKYSFTRDMLTHVRNTTGKPMFAVAFKNDLGAIENTLNKTSWNHSDVDPVPLHYNLYNA	300
ID	AAAY99602	standard; protein; 485 AA.		Db	241	IKYSFTRDMLTHVRNTTGKPMFAVAFKNDLGAIENTLNKTSWNHSDVDPVPLHYNLYNA	300
XX	AAAY99602;			Qy	301	SNSSGGYYDMENILNGSVVQKHPTHAVTFVDNHDSDQGEALSFVQWKFELAYALVLTRE	360
DT	04-SRP-2000	(first entry)		Db	301	SNSSGGYYDMENILNGSVVQKHPTHAVTFVDNHDSDQGEALSFVQWKFELAYALVLTRE	360
XX	Bacillus parent Termamyl-like alpha-amylase #1.			Qy	361	QGYPSVFYGDYIGIPTHGVPAKSKIDPLIQAQRTFAYGTQHDYFDHDDIIGHTREGNSS	420
DE	Bacillus;	alpha-amylase; washing; textile desizing; starch liquefaction;		Db	361	QGYPSVFYGDYIGIPTHGVPAKSKIDPLIQAQRTFAYGTQHDYFDHDDIIGHTREGNSS	420
KW	saccharification;	mutain; mutant; enzyme stability; hybrid.		Qy	421	HPNSGLATIMSDGPGGNKMYGKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480
XX	Bacillus sp.			Db	421	HPNSGLATIMSDGPGGNKMYGKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480
OS				Qy	481	VWVKQ 485	
XX	WO200029560-A1.			Db	481	VWVKQ 485	
PN							
XX	25-MAY-2000.						
XX	16-NOV-1999;	99WO-DK000628.					
PF	16-NOV-1998;	98DK-00001495.					
PR	(NOVO )	NOVO-NORDISK AS.					
XX	Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;						
PI	WPI; 2000-387777/33.						
XX	N-PSDB; AAA48480.						
DR	Variant of parent termamyl-like alpha amylase useful for washing, textile						
XX	desizing and starch liquefaction, comprising alterations in one or more						
PT	solvent exposed amino acid residues.						
XX	Claim 8; Page 53-54; 80pp; English.						
PS	The present sequence is a parent Termamyl-like alpha-amylase from which						
XX	mutants with increased stability at acidic pH, low calcium concentration						
CC	and high temperatures have been derived. The sequence encoding this						
CC	protein was isolated from a Bacillus genomic DNA library. A variant may						
CC	contain mutations in one or more solvent exposed amino acid residues to						
CC	increase the overall hydrophobicity of the enzyme or the overall number						
CC	of methyl groups in the side chain of exposed residues may be increased.						
CC	The mutations can be incorporated by site-directed mutagenesis or by						
CC	random mutagenesis. As a result of their increased stability, the						
CC	variants are suitable for the industrial processing of starch, i.e.						
CC	starch liquefaction and saccharification. They may also be useful for						
CC	washing, dishwashing and textile desizing. Hybrid alpha-amylases						
CC	comprising partial amino acid sequences derived from two or more alpha-						
CC	amylases have also been created in order to increase enzyme stability						
XX	Sequence 485 AA;						
SQ	Query Match	100.0%; Score 2714; DB 3; Length 485;					
	Best Local Similarity	100.0%; Pred. No. 1.1e-206;					
	Matches 485; Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	HHNGTGTMMQYFEWYLPNDGNHWRNLRDAAALKSKGITAVWIPPAWKGTQNDVGYGA	60				
Db	1	HHNGTGTMMQYFEWYLPNDGNHWRNLRDAAALKSKGITAVWIPPAWKGTQNDVGYGA	60				
Qy	61	YDLYDLGEFNGKQGTVRTKYGTRNLQAQAVTSLKNNGLQVYGDVVMNHKGGADGTEIVNAV	120				



CC groups in the side chains of exposed residues may be increased. The  
 CC mutations can be incorporated by site-directed mutagenesis or by random  
 CC mutagenesis. As a result of their increased stability, the variants are  
 CC suitable for the industrial processing of starch, i.e. starch  
 CC liquefaction and saccharification. They may also be useful for washing,  
 CC dishwashing and textile desizing. Hybrid alpha-amylases comprising  
 CC partial amino acid sequences derived from two or more alpha-amylases have  
 CC also been created in order to increase enzyme stability

XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 3; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLDAAANLKSIGITAVWIPPAWKGTSONDVGYGA 60  
 DB 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLDAAANLKSIGITAVWIPPAWKGTSONDVGYGA 60

QY 61 YDLVLDGEFNQKGVTRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
 DB 61 YDLVLDGEFNQKGVTRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120

QY 121 EVNRSNRNQTSGEYATIAEWTKDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180  
 DB 121 EVNRSNRNQTSGEYATIAEWTKDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTENGNYDYLMDVDMHPEVHELNRNGVWYTNLTLDGFRIDAVKH 240  
 DB 181 RGTGKAWDEVDTENGNYDYLMDVDMHPEVHELNRNGVWYTNLTLDGFRIDAVKH 240

QY 241 IKYSFTRDWLTHVRNTTGMKPFVAEFAEKNDLGAENYLNKTSWNHVSFVDFPLHNLNA 300  
 DB 241 IKYSFTRDWLTHVRNTTGMKPFVAEFAEKNDLGAENYLNKTSWNHVSFVDFPLHNLNA 300

QY 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSDQGEALSFVQWFKPLAYALVLTRE 360  
 DB 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSDQGEALSFVQWFKPLAYALVLTRE 360

QY 361 QGYPSPFYGYGYPGTHGVPAKSKIDPLQAROTFAYGTHQHDYFDHDIIGWTREGNSS 420  
 DB 361 QGYPSPFYGYGYPGTHGVPAKSKIDPLQAROTFAYGTHQHDYFDHDIIGWTREGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480  
 DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

QY 481 VVVKQ 485  
 DB 481 VVVKQ 485

RESULT 10  
 ABB06933  
 ID ABB06933 standard; protein; 485 AA.  
 XX  
 AC ABB06933;  
 XX  
 DT 19-JUN-2002 (first entry)  
 XX  
 DE Bacillus termamyl-like alpha-amylase protein SEQ ID NO:2.  
 XX  
 KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;  
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;  
 KW washing; sweetener; ethanol; starch.  
 XX  
 OS Bacillus sp.  
 XX  
 PN W0200166712-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 07-MAR-2001; 2001WO-DK000144.

XX 08-MAR-2000; 2000DK-00000376.  
 PR 15-MAR-2000; 2000US-0189857P.  
 PR 23-FEB-2001; 2001DK-00000303.  
 PR 26-FEB-2001; 2001US-0271382P.  
 XX (NOVO) NOVOZYMES AS.  
 XX Andersen C, Borchert TV, Nielsen BR;  
 FI WPI; 2002-239612/29.  
 DR N-PSDB; ABL50564.  
 DR  
 XX Novel variant of parent termamyl-like alpha-amylase useful as a component  
 PT in washing and dishwashing compositions, for textile desizing, for starch  
 PT liquefaction, and for producing sweeteners and ethanol from starch.  
 XX  
 PS Claim 8; Page 132-133; 153pp; English.  
 XX  
 CC The present invention describes a variant of a parent termamyl-like alpha  
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more  
 CC positions of a group of 31 possible amino acid positions. The alteration  
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,  
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,  
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,  
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for  
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.  
 CC (I) is useful as a component in hard surface cleaning detergent  
 CC composition, and for producing sweeteners and ethanol from starch. (I)  
 CC has altered solubility, preferably increased solubility, in particular  
 CC under washing, dish washing or hard surface cleaning conditions. The  
 CC present sequence represents a Bacillus termamyl-like alpha-amylase which  
 CC is used in the exemplification of the present invention  
 XX  
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 5; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLDAAANLKSIGITAVWIPPAWKGTSONDVGYGA 60  
 DB 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLDAAANLKSIGITAVWIPPAWKGTSONDVGYGA 60

QY 61 YDLVLDGEFNQKGVTRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
 DB 61 YDLVLDGEFNQKGVTRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120

QY 121 EVNRSNRNQTSGEYATIAEWTKDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180  
 DB 121 EVNRSNRNQTSGEYATIAEWTKDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTENGNYDYLMDVDMHPEVHELNRNGVWYTNLTLDGFRIDAVKH 240  
 DB 181 RGTGKAWDEVDTENGNYDYLMDVDMHPEVHELNRNGVWYTNLTLDGFRIDAVKH 240

QY 241 IKYSFTRDWLTHVRNTTGMKPFVAEFAEKNDLGAENYLNKTSWNHVSFVDFPLHNLNA 300  
 DB 241 IKYSFTRDWLTHVRNTTGMKPFVAEFAEKNDLGAENYLNKTSWNHVSFVDFPLHNLNA 300

QY 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSDQGEALSFVQWFKPLAYALVLTRE 360  
 DB 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSDQGEALSFVQWFKPLAYALVLTRE 360

QY 361 QGYPSPFYGYGYPGTHGVPAKSKIDPLQAROTFAYGTHQHDYFDHDIIGWTREGNSS 420  
 DB 361 QGYPSPFYGYGYPGTHGVPAKSKIDPLQAROTFAYGTHQHDYFDHDIIGWTREGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480  
 DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

QY 481 VVVKQ 485

[illegible]

CC kda has been provided. The product comprises a maltodextrin with a DE of  
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The  
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,  
 CC where the glucose syrup is useful as an ingredient in food, feed or  
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as  
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,  
 CC dairy and ice cream such as coffee whiteners, conventional foods such as  
 CC salad dressings, and food ingredients and preparations such as cured  
 CC meat, fermented meat, spices and seasoning encapsulated flavours  
 XX  
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 5; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HNGTNGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAATWIPPAWKGTSONDVGYGA 60  
 DB 1 HNGTNGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAATWIPPAWKGTSONDVGYGA 60  
 QY 61 YDLYDLGEFNGKQVTRTKYGRNQLAAVTSKNGIQVYGDVVMNHKGGADGTEIVNAV 120  
 DB 61 YDLYDLGEFNGKQVTRTKYGRNQLAAVTSKNGIQVYGDVVMNHKGGADGTEIVNAV 120  
 QY 121 EVNRSNRNQTSGEYAEAWTKFDFPGGRNNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
 DB 121 EVNRSNRNQTSGEYAEAWTKFDFPGGRNNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
 QY 181 RGTGKAWDEVDTEGNYDYLMDVDMHDPVHELNRNGVWYTNLTLDGFRIDAVKH 240  
 DB 181 RGTGKAWDEVDTEGNYDYLMDVDMHDPVHELNRNGVWYTNLTLDGFRIDAVKH 240  
 QY 241 IKYSFTRDLWTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNA 300  
 DB 241 IKYSFTRDLWTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNA 300  
 QY 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360  
 DB 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360  
 QY 361 QGTPSVFYGYIGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDIIGWTREGNSS 420  
 DB 361 QGTPSVFYGYIGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDIIGWTREGNSS 420  
 QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480  
 DB 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480  
 QY 481 VWVKQ 485  
 DB 481 VWVKQ 485

RESULT 13  
 ABB76586  
 ID ABB76586 standard; protein; 485 AA.  
 XX  
 AC ABB76586;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Termamyl-like-alpha-amylase #1.  
 XX  
 KW Termamyl; alpha amylase; starch liquefaction; ethanol production;  
 KW textile desizing; detergent; enzyme.  
 XX  
 OS Bacillus sp.  
 XX  
 PN WO200210355-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 12-JUL-2001; 2001WO-DK000488.

XX 01-AUG-2000; 2000DK-00001160.  
 PR 12-SEP-2000; 2000DK-00001354.  
 PR 10-NOV-2000; 2000DK-00001687.  
 PR 26-APR-2001; 2001DK-00000655.  
 XX (NOVO ) NOVOZYMES AS.  
 PA Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;  
 XX  
 XX WPI; 2002-280633/32.  
 DR N-PSDB; ABL96207.  
 XX  
 PT Variant of parent Termamyl-like alpha amylase, useful in detergent  
 PT compositions, for starch liquefaction, ethanol production, washing and/or  
 PT dish washing, and textile desizing.  
 XX  
 PS Claim 8; Fig 2; 90pp; English.  
 XX  
 CC This invention relates to variants of a parent Termamyl-like alpha-  
 CC amylases. These are used for starch liquefaction, ethanol production,  
 CC detergent, and textile desizing. The amylases have altered stability,  
 CC particularly at high temperatures from 70-120plusoc and low pH in the  
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-  
 CC amylase  
 XX  
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 5; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HNGTNGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAATWIPPAWKGTSONDVGYGA 60  
 DB 1 HNGTNGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAATWIPPAWKGTSONDVGYGA 60  
 QY 61 YDLYDLGEFNGKQVTRTKYGRNQLAAVTSKNGIQVYGDVVMNHKGGADGTEIVNAV 120  
 DB 61 YDLYDLGEFNGKQVTRTKYGRNQLAAVTSKNGIQVYGDVVMNHKGGADGTEIVNAV 120  
 QY 121 EVNRSNRNQTSGEYAEAWTKFDFPGGRNNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
 DB 121 EVNRSNRNQTSGEYAEAWTKFDFPGGRNNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
 QY 181 RGTGKAWDEVDTEGNYDYLMDVDMHDPVHELNRNGVWYTNLTLDGFRIDAVKH 240  
 DB 181 RGTGKAWDEVDTEGNYDYLMDVDMHDPVHELNRNGVWYTNLTLDGFRIDAVKH 240  
 QY 241 IKYSFTRDLWTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNA 300  
 DB 241 IKYSFTRDLWTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNA 300  
 QY 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360  
 DB 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360  
 QY 361 QGTPSVFYGYIGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDIIGWTREGNSS 420  
 DB 361 QGTPSVFYGYIGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDIIGWTREGNSS 420  
 QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480  
 DB 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480  
 QY 481 VWVKQ 485  
 DB 481 VWVKQ 485  
 RESULT 14  
 ABB99480  
 ID ABB99480 standard; protein; 485 AA.  
 XX



CC also be used in the production of sweeteners and ethanol from starch

XX Sequence 485 AA;

Query Match 99.9%; Score 2712; DB 2; Length 485;  
Best Local Similarity 99.8%; Pred. No. 1.6e-206;  
Matches 484; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HHNGTNGTMQYFHWYLPNDGNHNRRLRDDAANKSGKITAVIPPAWKGTSONDVGGA	60
Db	1	HHNGTNGTMQYFHWYLPNDGNHNRRLRDDAANKSGKITAVIPPAWKGTSONDVGGA	60
Qy	61	YDLVDLGEFNQKGTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVVNNHKGAGDGTETVNAV	120
Db	61	YDLVDLGEFNQKGTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVVNNHKGAGDGTETVNAV	120
Qy	121	EVNRSNRNQETSGEYAEAWTKFDFPGRGNNHSHFKWRWHYHFDGTDWDQSRQLQNKIYKF	180
Db	121	EVNRSNRNQETSGEYAEAWTKFDFPGRGNNHSHFKWRWHYHFDGTDWDQSRQLQNKIYKF	180
Qy	181	RGTCKAWDWEVDTEGNYDYLMYADVDMDHPEVIHELNNGWVWYTTNTLNLDFRIDAVKH	240
Db	181	RGTCKAWDWEVDTEGNYDYLMYADVDMDHPEVIHELNNGWVWYTTNTLNLDFRIDAVKH	240
Qy	241	IKYSFTRDWLTHVRNTTGKPMFAVAEPWKNLDLGAIENTYLNKTSWNHSHVDFVPLHYNLYNA	300
Db	241	IKYSFTRDWLTHVRNTTGKPMFAVAEPWKNLDLGAIENTYLNKTSWNHSHVDFVPLHYNLYNA	300
Qy	301	SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQOWFKPLAYALVLTRE	360
Db	301	SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQOWFKPLAYALVLTRE	360
Qy	361	QGYPSVFYGDYIGIPTHGVPAMKSKIDPLLQARQTFAYGTQHDYFDHHDIIIGWTREGNSS	420
Db	361	QGYPSVFYGDYIGIPTHGVPAMKSKIDPLLQARQTFAYGTQHDYFDHHDIIIGWTREGNSS	420
Qy	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480
Db	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480
Qy	481	VWKQ 485	
Db	481	VWKQ 485	

Search completed: October 7, 2004, 00:12:11  
Job time : 62.5516 secs

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.886 Seconds  
(without alignments)  
3134.012 Million cell updates/sec

Title: US-09-925-576C-2

Perfect score: 2714

Sequence: 1 HHNGTNGTMMQYFEWYLPND.....ADGKGNFVNGSGSVVWKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2440	89.9	518	1 A27705	alpha-amylase (EC
2	1909.5	70.4	549	1 A54541	alpha-amylase (EC
3	1905	70.2	512	1 ALBSL	alpha-amylase (EC
4	1898.5	70.0	549	1 A24549	alpha-amylase (EC
5	1892.5	69.7	549	1 A24436	alpha-amylase (EC
6	1850	68.2	514	1 ALBSN	alpha-amylase (EC
7	1831	67.5	548	1 ALBSF	alpha-amylase (EC
8	1344	49.5	493	2 S15713	alpha-amylase (EC
9	1245	45.9	484	2 G95160	alpha-amylase (imp
10	1243	45.8	484	2 F98026	alpha-amylase (EC
11	1239	45.7	492	2 AH2079	alpha-amylase (imp
12	1127	41.5	491	2 C86781	alpha-amylase (imp
13	1097	40.4	506	2 G98247	cytoplasmic alpha-
14	1096	40.4	495	2 AD3038	alpha-amylase (EC
15	1076	39.6	494	1 B45738	alpha-amylase (EC
16	1066	39.3	494	2 AD0751	cytoplasmic alpha-
17	1054	38.8	495	2 B90962	cytoplasmic alpha-
18	1049	38.7	495	1 A45738	alpha-amylase (EC
19	1035	38.1	495	2 B85810	cytoplasmic alpha-
20	382.5	14.1	217	2 AL9S06	alpha-amylase (EC
21	316	11.6	1196	2 A29130	beta-amylase (EC 3
22	305.5	11.3	421	2 S10514	alpha-amylase (EC
23	295.5	10.9	482	2 S31478	alpha-amylase (EC
24	294	10.8	440	2 S14958	alpha-amylase (EC
25	289.5	10.7	551	2 S05667	glucan 1,4-alpha-m
26	288	10.6	423	2 T09942	alpha-amylase (EC
27	285.5	10.5	826	2 E96720	probable alpha-amy
28	274.5	10.1	547	2 A32803	glucan 1,4-alpha-m
29	274	10.1	428	2 T05521	alpha-amylase (EC

#### RESULT 1

A27705

alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase

C;Species: Bacillus sp.

C;Date: 31-Mar-1989 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999

C;Accession: A27705

E;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.

Biochem. Biophys. Res. Commun. 151, 25-31, 1988

A;Title: Nucleotide sequence of the maltohexaose-producing amylase gene from an alkaloph

A;Reference number: A27705; MUID:88162814; PMID:3258152

A;Accession: A27705

A;Molecule type: DNA

A;Residues: 1-518 <TSU>

A;Cross-references: GB:M18862; NID:g142496; PID:AAA22231.1; PID:g142497

A;Experimental source: chromosomal DNA of strain 707

A;Note: amino end of mature protein also determined

C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amyliofaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F;1-33/Domains: signal sequence #status predicted <SIG>

F;34-518/Product: alpha-amylase #status experimental <MAT>

F;236-369/Domains: alpha-amylase core homology <AMY>

F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted

F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 89.9%; Score 2440; DB 1; Length 518;

Best Local Similarity 87.6%; Pred. No. 4.1e-157; Indels 0; Gaps 0;

Matches 425; Conservative 32; Mismatches 28;

Qy 1 HHNGTNGTMMQYFEWYLPNDGNHWNRLRDAANLKSXGITAIVTTPPAWKGTSONDVGYGA 60

Db 34 HHNGTNGTMMQYFEWYLPNDGNHWNRLNSDASNLKSXGITAIVTTPPAWKGSQNDVGYGA 93

Qy 61 YDLVDFEFNQKGVTRTKYGTNRNQLQAATVSLKNGGQVYGVGVVNNHKGSGADGTETVNAV 120

Db 94 YDLVDFEFNQKGVTRTKYGTNRSLQAATVSLKNGGQVYGVGVVNNHKGSGADATETVNAV 153

Qy 121 EVNRSNNOETSGEYATEAWTKDFPGKNNHSSFKRWVHFDGTDQSDQSLQNKLYKF 180

Db 154 EVNPNNNQEVGTGYTTEAWTRFDGKNNHSSFKRWVHFDGVDMDQSLNNRIYKF 213

Qy 181 RGTGKAWDEVDTEGNGYDILMYADVDMDHPEVTHELRNMGVWYTNLTLDGFRIDAVKH 240

Db 214 RGHGKAWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTLDGFRIDAVKH 273

Qy 241 IKYSFTRDWLTHTVNTTKGKMPFAVAEPKNDLGAIEYLNKTSWNHVSFVDFPLHYNLYNA 300

Db 274 IKYSFTRDWINHVSATGKNMFAVAEPKNDLGAIEYLNKTSWNHVSFVDFPLHYNLYNA 333

QY	301	SNSGYGYDMRNILNGSVVQKHPTHTAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE	360
Db	334	SKSGGNYDMRNINFGTVQQRPHSHAVTFVDNHDSDQGEALESFVEWFKPLAYALTIRE	393
QY	361	QGYPSVFYGYDYGIPTHGVPAKMSKIDPLLOARQTFAYGTQHDYFDHDIIGWTRGNSG	420
Db	394	QGYPSVFYGYDYGIPTHGVPAKMSKIDPILAEARKVAYKQNDYLDHNIIGWTRGNTA	453
QY	421	HPNSGLATIMSDPGGNKMYVGNKAGQWRDITGNRTGTVTNADGWNFSVNGGSVS	480
Db	454	HPNSGLATIMSDGAGGSKMVFGRNKGQVMSDITGNRTGTVTNADGWNFSVNGGSVS	513
QY	481	VWYKQ 485	
Db	514	IWNK 518	
RESULT 2			
A54541			
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI1792)			
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase			
C;Species: Bacillus stearothermophilus			
C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997			
C;Accession: A54541			
R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.			
FEMS Microbiol. Lett. 77, 271-276, 1991			
A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.			
A;Reference number: A54541			
A;Accession: A54541			
A;Molecule type: DNA			
A;Residues: 1-549 <TOR>			
A;Cross-references: GB:X59476			
A;Experimental source: Chromosomal DNA of strain DNI1792			
C;Comment: Alpha-amylase Genes have been found on plasmids and in multiple copies on the			
C;Genetics:			
A;Start codon: GTG			
C;Function:			
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds			
A;Pathway: glycogen/starch degradation			
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology			
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac			
F;1-34/Domain: signal sequence #status predicted <SIG>			
F;35-549/Product: alpha-amylase #status predicted <MAT>			
F;235-368/Domain: alpha-amylase core homology <AMY>			
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted			
F;268,298,365/Active site: Asp, Glu, Asp #status predicted			
Query Match 70.4%; Score 1909.5; DB 1; Length 549;			
Best Local Similarity 68.6%; Pred. No. 2.7e-121;			
Matches 328; Conservative 69; Mismatches 80; Indels 1; Gaps 1;			
QY	6	NGTMQYFEWYLPNDGNHNRDLDDAANLKSKITAVWIPPAKGTSONDVGGAYDLYD	65
Db	39	NGTMQYFEWYLPDGLTWTKVANEANNLSSGITALWLPAYKGTSRSDVGGVYDLYD	98
QY	66	LGSEFNQGTVRTKYGRFNQLQAAVTSLKXNGIOVYGDVNMVHKGAGDTGTVNAVEVNR	125
Db	99	LGSEFNQGTVRTKYGTAKQYLOIAQAAHAGQVYADVFDHKGAGDTGTVDAVEVNP	158
QY	126	NRNQETSGEYAIBAWTKFDPFGRGNHSSPKRWYHFDGTDWQSRQLQNKYIKFRGTGK	185
Db	159	DRNQEISGTYQIQAWTKFDPFGRGNTYSSPKRWYHFDGVDWDESRL-SRIYKFRGIGK	217
QY	186	AWDEVDVTENGNDYLMYADVMDHDEVIHELNRNGWYNTNLNLDGFRIDAVKHLYKSF	245
Db	218	AWDEVDVTENGNDYLMYADLDMDHPEVTELNKNGKWYNTNIDGFRIDAVKHLYKSF	277
QY	246	TRDLVTHVRTKGPFAVAEFWKNDLGAJENYLNKTSWNHVSFDPVPLHVNLYNAGNSG	305
Db	278	FPDLVSVRSGTKPLFTVEGYNSYDINKLHNITKTDGTMSLFDAPLHNKFTASKSG	337
QY	306	YDMRNILNGSVVQKHPTHTAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTREOGYPS	365

Db	338	APDMRTLMTNLMKQDPTLAVTFVDNHDTEPGQALQSWDWPFKPLAYAFILTRQEGYPC	397
QY	366	VFYGDYDYGIPTHGVPAKMSKIDPLLOARQTFAYGTQHDYFDHDIIGWTRGNSHNSG	425
Db	398	VFYGDYDYGIPQVNPISPKSKIDPLLIARRDAYGTQHDYLDHSDIIGWTRGGGTERKPGSG	457
QY	426	LATIMSDGPGGNKMYVGNKAGQWRDITGNRTGTVTNADGWNFSVNGGSVSVMV	483
Db	458	LAALITDGPGGSKMYVGNKAGKVFYDLTGNRSDITVINSDDGWBKFNKNGSSVSMV	515
RESULT 3			
ALBSL			
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis			
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase			
C;Species: Bacillus licheniformis			
C;Date: 30-Jun-1987 #sequence_revision 24-Apr-1998 #text_change 15-Sep-2000			
C;Accession: A91997; B24549; A91796; A21663; I39772; I39772; A26151; S53788; A00844			
R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.			
J. Biochem. 98, 1147-1156, 1985			
A;Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amyl			
ases deduced from the DNA sequences.			
A;Reference number: A91997; MUID:86111694; PMID:2418011			
A;Accession: A91997			
A;Molecule type: DNA			
A;Residues: 1-162, 'R', 164-512 <YU>			
A;Cross-references: GB:X03236; NID:G39551; PIDN:CRA26981.1; PID:G39552			
A;Experimental source: ATCC 27811			
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt,			
J. Bacteriol. 166, 635-643, 1986			
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearotherm			
A;Reference number: A91817; MUID:86195857; PMID:3009417			
A;Accession: B24549			
A;Molecule type: DNA			
A;Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>			
A;Cross-references: GB:M13256; NID:G142510; PIDN:AAA22240.1; PID:G142511			
A;Experimental source: NCIB 8061			
R;Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.			
J. Bacteriol. 158, 369-372, 1984			
A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase			
A;Reference number: A91796; MUID:84185455; PMID:6609154			
A;Accession: A91796			
A;Molecule type: DNA			
A;Residues: 1-104 <STE>			
A;Cross-references: GB:K01984; NID:G142432; PIDN:AAA22193.1; PID:G142433			
R;Sibakov, M.; Palva, I.			
Eur. J. Biochem. 145, 567-572, 1984			
A;Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-am			
A;Reference number: A21663; MUID:85076654; PMID:6334606			
A;Accession: A21663			
A;Molecule type: DNA			
A;Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 81			
A;Experimental source: Chromosomal DNA of ATCC 14580			
A;Note: the authors translated the codon CGR for residue 48 as Gly and GAC for residue 6			
R;Laoid, B.M.; Chambliss, G.H.; McConnell, D.J.			
J. Bacteriol. 171, 2435-2442, 1989			
A;Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent			
A;Reference number: I39773; MUID:89213924; PMID:2540150			
A;Accession: I39774			
A;Status: translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-29 <LAO>			
A;Cross-references: GB:M26412; NID:G341477; PIDN:AAA2237.1; PID:G516590			
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.			
Gene 96, 37-41, 1990			
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con			
A;Reference number: I39772; MUID:91092499; PMID:2265757			
A;Accession: I39772			
A;Status: translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-32, 'I' <TOR>			
A;Cross-references: GB:M62637; NID:G142498; PIDN:AAA22232.1; PID:G142499			



R;Kuhn, H.; Fietzek, P.P.; Lampen, J.O.  
J. Bacteriol. 149, 372-373, 1982  
A:Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison  
A:Reference number: A26151; MUID:82098050; PMID:6172418  
A:Accession: A26151  
A:Molecule type: protein  
A:Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>  
R;Machius, M.; Wiegand, G.; Huber, R.  
J. Mol. Biol. 246, 545-559, 1995  
A:Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2  
A:Reference number: S53788; MUID:95182462; PMID:7877175  
A:Accession: S53788  
A:Molecule type: protein  
A:Residues: D', 220-227 <MAC>  
A:Note: sequence represents amino end of an internal fragment created by a single enzyme  
R;Machius, M.; Wiegand, G.; Huber, R.  
Submitted to the Brookhaven Protein Data Bank, July 1995  
A:Reference number: A65206; PDB:1BPL  
A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210,222-511  
R;Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.  
Submitted to the Brookhaven Protein Data Bank, October 1996  
A:Reference number: A66860; PDB:1VUS  
A:Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210,222-511  
C:Genetics:  
A:Gene: amyl  
C:Function:  
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A:Pathway: glycogen/starch degradation  
A:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac  
F;1-29/Domains: signal sequence #status predicted <SIG>  
F;30-512/Product: alpha-amylase #status experimental <AMY>  
F;227-360/Domains: alpha-amylase core homology <AMY>  
F;133,229,264/Binding site: calcium (Asn, Asp, His) #status experimental  
F;260,290,357/Active site: Asp, Glu, Asp #status experimental  
Query Match 70.2%; Score 1905; DB 1; Length 512;  
Best Local Similarity 68.9%; Pred. No. 5e-121;  
Matches 334; Conservative 65; Mismatches 76; Indels 10; Gaps 4;  
Qy 6 NGTMMQFVFWLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSQNDVGYGAYDLYD 65  
Db 33 NGTMMQFVFWLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSQNDVGYGAYDLYD 92  
Qy 66 LGFENQKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVDMVNMHKGADGTEIVNAVEVNR 125  
Db 93 LGFENQKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVDMVNMHKGADGTEIVNAVEVNR 152  
Qy 126 NRNQETSGEYAEIAWTKDFPGRGNHSSFKRWYHFDGTDQOSQRLQNKIYKFRGTGK 185  
Db 153 DRNRVISGEHLIKAWTHFHPGRGSTYDFKWHYHFDGTDQOSQRLQNKIYKFRGTGK 209  
Qy 186 AWDDEVDTENGNDYLMYADVMDHPEVIELRNWGVYNTNLNDGFRIDAVKHIXYF 245  
Db 210 AWDDEVDTENGNDYLMYADVMDHPEVIELRNWGVYNTNLNDGFRIDAVKHIXYF 269  
Qy 246 TRDWLTHVRNTTKPMFAVAFWKNLGAENYLNKTSWNHVSFDPVPLHYNLYNASNGG 305  
Db 270 LRDMVNHVREKTKGEMFTVAEYQNDLGAENYLNKTSWNHVSFDPVPLHYNLYNASNGG 329  
Qy 306 YYDMRNILNGSVQKHPHTAVTFVDNHDSDQGEALSGFVQWFKPLAYALVLTREQGYPS 365  
Db 330 GYDMKLLNSTVSKHPLKAVTFVDNHDSDQGEALSGFVQWFKPLAYALVLTREQGYPS 389  
Qy 366 VFYGDYGIPTHG-----VPAMKSKIDPLLAQRTQAYGTDHHDHIGWTRGNSG 420  
Db 390 VFYGDYGIPTHG-----VPAMKSKIDPLLAQRTQAYGTDHHDHIGWTRGNSG 447  
Qy 421 HPNSGLATIMSDGGGKNKMYVGNKAGQWRDITGNRTGTVTINADGWNFSVNGSGVS 480  
Db 448 VANSGLAALITDGGPGKARMYVGRQNAGETWHDTIGNRSEPVVINSWGGEFHYNGSGVS 507

Qy 481 VVWKQ 485  
Db 508 IYVQR 512  
RESULT 4  
A24549  
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)  
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C:Species: Bacillus stearothermophilus  
C:Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text\_change 18-Jun-1999  
C:Accession: A24549; I39501; I39770  
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requadt,  
J. Bacteriol. 166, 635-643, 1986  
A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothe  
A:Reference number: A91817; MUID:86195857; PMID:3009417  
A:Accession: A24549  
A:Molecule type: DNA  
A:Residues: 1-549 <GRA>  
A:Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513  
A:Experimental source: genomic DNA of strain NZ-3  
R;Sato, H.; Nishida, H.; Isono, K.  
J. Bacteriol. 170, 1034-1040, 1988  
A:Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista  
A:Reference number: I39501; MUID:88139156; PMID:3257753  
A:Accession: I39501  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 536-549 <RES>  
A:Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478  
A:Experimental source: strain DY-5  
A:Accession: I39770  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 536-549 <RE2>  
A:Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486  
A:Experimental source: strain 799  
C:Genetics:  
A:Start codon: GTG  
C:Function:  
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A:Pathway: glycogen/starch degradation  
A:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac  
F;1-34/Domains: signal sequence #status predicted <SIG>  
F;35-549/Product: alpha-amylase #status predicted <MAT>  
F;235-368/Domains: alpha-amylase core homology <AMY>  
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted  
F;268,298,365/Active site: Asp, Glu, Asp #status predicted  
Query Match 70.0%; Score 1898.5; DB 1; Length 549;  
Best Local Similarity 68.4%; Pred. No. 1.5e-120;  
Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;  
Qy 6 NGTMMQFVFWLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSQNDVGYGAYDLYD 65  
Db 39 NGTMMQFVFWLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSQNDVGYGAYDLYD 98  
Qy 66 LGFENQKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVDMVNMHKGADGTEIVNAVEVNR 125  
Db 99 LGFENQKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVDMVNMHKGADGTEIVNAVEVNR 158  
Qy 126 NRNQETSGEYAEIAWTKDFPGRGNHSSFKRWYHFDGTDQOSQRLQNKIYKFRGTGK 185  
Db 159 DRNQETSGEYAEIAWTKDFPGRGNHSSFKRWYHFDGTDQOSQRLQNKIYKFRGTGK 217  
Qy 186 AWDDEVDTENGNDYLMYADVMDHPEVIELRNWGVYNTNLNDGFRIDAVKHIXYF 245  
Db 218 AWDDEVDTENGNDYLMYADVMDHPEVIELRNWGVYNTNLNDGFRIDAVKHIXYF 277  
Qy 246 TRDWLTHVRNTTKPMFAVAFWKNLGAENYLNKTSWNHVSFDPVPLHYNLYNASNGG 305

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Db      278  FPDWLSYVRSGTQKPLFTVEYWSYDINKLHNYITTKNGTMSLFDAPLHNKFTASKSGG 337
QY      306  YDMRNLINGSVQKPTHTAVTFVDNHDSPGSALESFVQWFKPLAYALVLTREQGYPS 365
Db      338  AFMSILMNTLWKDQPTLAVTFVDNHDTEPGALQSWDPWFKPLAYAFILTRQSGYPC 397
QY      366  VFYGDYGIPTGTHGVPAWMSKIDPQLQAROTFAYGTQHDYFDHDDIIGWTREGNSSHPNSG 425
Db      398  VFYGDYGIPTGTHGVPAWMSKIDPQLQAROTFAYGTQHDYFDHDDIIGWTREGVTEKPGSG 457
QY      426  LATIMSDGPGGNKMWYGVKNAQGVWRDITGNRTGTVTINADGWGNSFVNGSVSVWV 483
Db      458  LAALITDGGGSKMWYGVKQHAGKVFYDLTGNSRSDVTITNSDGGWGFKNVGGSVSVWV 515

RESULT 5
A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24436; I39777
R;Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A;Reference number: A24436; MUID:85234394; PMID:3924897
A;Accession: A24436
A;Molecule type: DNA
A;Residues: 1-549 <NA>
A;Cross-references: GB:M11450
A;Experimental source: plasmid pAT5
A;Note: amino end of the mature protein also determined
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A;Reference number: I39772; MUID:91092499; PMID:2465757
A;Accession: I39777
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-45 <RES>
A;Cross-references: GB:M62638; NID:gl42514; PIDN:AAA2242.1; PID:gl42515
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Gene: amyS
A;Genome: plasmid
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
F;1-34/Domain: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
F;35-549/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <MAT>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match          69.7%; Score 1892.5; DB 1; Length 549;
Best Local Similarity 68.2%; Pred. No. 3.8e-120;
Matches 32e; Conservative 70; Mismatches 81; Indels 1; Gaps 1;

QY      6  NGTMMQYFEWYLPDNGNHNRLRDLDAANLKSIGITAWIPPAWKGTSONDVGYGAYDLYD 65
Db      39  NGTMMQYFEWYLPDGTGLTWKVAENANLSSIGITALLWLPYKGTSRSDVGYGVYDLYD 98
QY      66  LGFBNOKGTVRTYKTRNLQAAVTSLKNNGIQYGDVWVWNNHKGADGTIVNAVEVNRS 125
Db      99  LGFBNOKGAVRTYKGTAKQYLOIAHAAGMQVYADVDFHKGADGTWVDVAEVPNS 158
QY      126  NRNQETSGEVAIEAWTKFDPGPGNNHSSPKRWYHFDGTDWQSRQLOMKYKFRGTGK 185
Db      159  DRNQELSGTYQIQAWTKFDPGPGNNYSSPKRWYHFDGVDWDESKL-SRIYKFRGIGK 217
QY      186  AWDWEVDVTENGNYDLYMADVDMDHPEVIHELNRWGWYVTNTNLNLDGFRIDAVKHKYSF 245

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Db      218  AWDWEVDVTENGNYDLYMADVDMDHPEVVTLSKWKGVYVTNTNIDGFRIDAVKHKFSF 277
QY      246  TRDMLTHVNTTCKPMFAVAFKNDLGALENLNTKSNHNSVDFVPLHYNLNASNSGG 305
Db      278  FPDWLSYVRSGTQKPLFTVEYWSYDINKLHNYITTKNGTMSLFDAPLHNKFTASKSGG 337
QY      306  YDMRNLINGSVQKPTHTAVTFVDNHDSPGSALESFVQWFKPLAYALVLTREQGYPS 365
Db      338  FPDWLSYVRSGTQKPLFTVEYWSYDINKLHNYITTKNGTMSLFDAPLHNKFTASKSGG 397
QY      366  VFYGDYGIPTGTHGVPAWMSKIDPQLQAROTFAYGTQHDYFDHDDIIGWTREGNSSHPNSG 425
Db      398  VFYGDYGIPTGTHGVPAWMSKIDPQLQAROTFAYGTQHDYFDHDDIIGWTREGVTEKPGSG 457
QY      426  LATIMSDGPGGNKMWYGVKNAQGVWRDITGNRTGTVTINADGWGNSFVNGSVSVWV 483
Db      458  LAALITDGGGSKMWYGVKQHAGKVFYDLTGNSRSDVTITNSDGGWGFKNVGGSVSVWV 515

RESULT 6
ALASN
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus amylioliquefaciens
C;Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
C;Accession: A92389; I39756; I39763; A00843
R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
J. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced fr
A;Reference number: A92389; MUID:83108808; PMID:6185474
A;Contents: PUB110
A;Accession: A92389
A;Molecule type: DNA
A;Residues: 1-514 <TAK>
A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:gl42428; PIDN:AAA2219
R;Chung, H.S.; Friedberg, F.
Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.
A;Reference number: A90307; MUID:80241725; PMID:6156671
A;Accession: A90307
A;Molecule type: protein
A;Residues: 32-53,'I',55-63,'I',65-78,'D',80-83,'S',85-222 <CHU>
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of th
A;Reference number: I39756; MUID:82051296; PMID:6170539
A;Accession: I39756
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-96 <RES>
A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karanen, S.
Gene 59, 161-170, 1987
A;Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its own
A;Reference number: I39763; MUID:88137952; PMID:2830166
A;Accession: I39763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-39 <RES>
A;Cross-references: GB:M18424; NID:gl42430; PIDN:AAA22192.1; PID:gl42431
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-514/Product: alpha-amylase #status predicted <AMT>
F;229-362/Domain: alpha-amylase core homology <AMT>
F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F;262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match          68.2%; Score 1850; DB 1; Length 514;

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A;Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:gl15159379; GSPDB:GN00170  
C;Genetics:  
A;Gene: AGR L 1863  
A;Map position: linear chromosome  
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 40.4%; Score 1097; DB 2; Length 506;  
Best Local Similarity 45.1%; Pred. No. 1.6e-66;  
Matches 223; Conservative 76; Mismatches 178; Indels 18; Gaps 7;

QY 3 NGTNGTMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSON-DVGYGAY 61  
DB 11 NMAGRITLQPFHWYYPDGGKLSWAEKASLAKMGITDVLWLPAYKAAGSVGYDY 70  
QY 62 DLYDLGEFNQKGVTRTKYGRNLOQAAVTSLKNNGIQVYGDVVMNHKGGADGTEIYNAVE 121  
DB 71 DLFDLGEFDQGVATKYGDRAALEHAGKTLKONGIRVHDVVLNHNKGADEKEKVRVR 130  
QY 122 VNRNRNQETSGRYAIEAWTKFDPGRGNHNSFKRWYHFDGTDWDSRQLQNKIYKF- 180  
DB 131 VNPDDRDIIDEDFPALAYTRFTFPGRNKGHSKFIWDLKCFSGVDHIE-EPTEDGIFRLV 189  
QY 181 --RGTKANDWEVDTENGNDYLYADVDMDHPEVHELNRNKGWVYTNLNDGPRIDAV 238  
DB 190 NEYGDGE-WNEEVDQENGFYDLMGADVEFRNRAVYELKYWGRWLSQVQVDDGFLDAA 248  
QY 239 KHLKYSFTRDLWLTNRNTTKPMFAVAEFKNDLGAENYLNKTSWNHVSFVDPVPLHNYLY 298  
DB 249 KHLPAWFFRDVWGHMRETVDPLFVVAEYVHPDLEALKSYLELVQKLMFLDVALHHSFH 308  
QY 299 NASNSGGYYDMRNILNGSVQKHPTHAFTVDNHDSPQGEALSFVQOWFKPLAYALVLT 358  
DB 309 DASKQGGDFMRSIFDGLSVAPDHAFTLVNDHDTQPLQSLAPVPEWPKPLAYAILL 368  
QY 359 REOGYPSVFGDYVG--IPTHGVPAKSKID-----PLLOAROTFAYGTQHDYFDHH 408  
DB 369 REEGVPCVFYFDLFGTSYDTGTGNDGNEYKIDIPAIECLPKLIEARSFANGPQTDFDDA 428  
QY 409 DIIGTWREGNSHPNSGLATIMSDGPGKNKMWYVGNKAGQVWRDITGNRTGTVTINADG 468  
DB 429 SCTAFIRHGTADAP--GCVVMSNGEPGEQADLGPERSAGVWRDFLGHRHEHITLDESG 486  
QY 469 WGNFNSVNGGSVSVWV 483  
DB 487 KGTFFPINGGSVSVWV 501

RESULT 14  
AD3038  
alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C;Accession: AD3038  
R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I.  
erage, G.; Gilet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AD3038  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-495 <KUR>  
A;Cross-references: GB:AE008689; PIDN:AAI44722.1; PID:gl17742354; GSPDB:GN00187  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: amyA  
A;Map position: linear chromosome  
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 40.4%; Score 1096; DB 2; Length 495;

Best Local Similarity 45.3%; Pred. No. 1.8e-66;  
Matches 222; Conservative 76; Mismatches 174; Indels 18; Gaps 7;

QY 8 TMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSON-DVGYGAYDYL 66  
DB 5 TULQFHHWYYPDGGKLSWAEKASLAKMGITDVLWLPAYKAAGSVGYDYDLDL 64  
QY 67 GBFNQKGVTRTKYGRNLOQAAVTSLKNNGIQVYGDVVMNHKGGADGTEIYNAVEVNRN 126  
DB 65 GSFQDKGTATKYGDRAALEHAGKTLKONGIRVHDVVLNHNKGADEKEKVRVRVNPDD 124  
QY 127 RQETSGEVAIEAWTKFDPGRGNHNSFKRWYHFDGTDWDSRQLQNKIYKF---RGT 183  
DB 125 RTDIDDEDPPALAYTRFTFPGRNKGHSKFIWDLKCFSGVDHIE-EPTEDGIFRLVNEYGD 183  
QY 184 GKAWDEWVDTENGNDYLYADVDMDHPEVHELNRNKGWVYTNLNDGPRIDAVKHXY 243  
DB 184 GE-WNEEVDQENGFYDLMGADVEFRNRAVYELKYWGRWLSQVQVDDGFLDAAHIPA 242  
QY 244 SFTRWLTNRNTTKPMFAVAEFKNDLGAENYLNKTSWNHVSFVDPVPLHNYLYNASNS 303  
DB 243 WFFRDVWGHMRETVDPLFVVAEYVHPDLEALKSYLELVQKLMFLDVALHHSFHDASKQ 302  
QY 304 GGYDMRNILNGSVQKHPTHAFTVDNHDSPQGEALSFVQOWFKPLAYALVLTREOGY 363  
DB 303 GGDFFMRSIFDGLSVAPDHAFTLVNDHDTQPLQSLAPVPEWPKPLAYAILLREEGV 362  
QY 364 PSVFYGDYVG--IPTHGVPAKSKID-----PLLOAROTFAYGTQHDYFDHDIIGW 413  
DB 363 PCVFYFDLFGTSYDTGTGNDGNEYKIDIPAIECLPKLIEARSFANGPQTDFDDASCIAP 422  
QY 414 TREGNSHPNSGLATIMSDGPGKNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFS 473  
DB 423 IRHGTADAP--GCVVMSNGEPGEQADLGPERSAGVWRDFLCHREHITLDESGKGTGP 480  
QY 474 VNGGSVSVWV 483  
DB 481 TNGGSVSVWV 490

RESULT 15  
B45738  
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium  
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C;Species: Salmonella typhimurium  
C;Date: 07-Apr-1994 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
C;Accession: B45738  
R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.  
J. Bacteriol. 174, 6644-6652, 1992  
A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.  
A;Reference number: A45738; MUID:93015717; PMID:1400215  
A;Accession: B45738  
A;Molecule type: DNA  
A;Residues: 1-494 <RAH>  
A;Cross-references: GB:I01643; NID:gl54043; PIDN:AAA27110.1; PID:gl54045  
C;Genetics:  
A;Gene: amyA  
A;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
C;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology  
C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation  
F;202-335/Domain: alpha-amylase core homology <AMY>  
F;239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.6%; Score 1076; DB 1; Length 494;  
Best Local Similarity 42.7%; Pred. No. 4e-65;  
Matches 210; Conservative 81; Mismatches 183; Indels 18; Gaps 6;

QY 6 NGTMOYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSON-DVGYGAYDYL 64  
DB 3 NPTLLQYFHWYYPDGGKLSWAEKASLAKMGITDVLWLPAYKAAGSVGYDYDYL 62

Qy	65	DLGEFNOKGTVRTKYGTNRNLOAAVTSLNKNGIQYIGDVVNMHKGADGTETVNAVEVNR	124
Db	63	DLGEFDQKGTATATKYGDKRQLLTALDALKNNIAVLLDVVNMHKGADKERRIRVQRVNO	122
Qy	125	SNRQETISGEVAIEAWTKFDPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKFRG--	182
Db	123	DDRTQIDDNIIIECGWTRYTPPARAGQYSNFIDYHCFSGIDHIENPD-EDGIFKI VNDY	181
Qy	183	TGKAWDMEVDTPENGNYDYLYMADYDMDHPEVIHEL RNWGVWYTTNTLNL DGFRI DAVKH I K	242
Db	182	TGDCWNDQVDDMGNFYDLNGENIDFRNHAVTEI KYWAWVMEQTHCDGFRLD AVKH I P	241
Qy	243	YSFTRDMLTHVRNTTGKPMFAVEFWKNDLGAIENYLNKTSWNHVSFVPLHYNLYNASN	302
Db	242	AWFYKEMIEHVQAVAPKPLFTVAEYWSHEVDKLTQYIDQVDGKTMLFDAPLQMKFHEASR	301
Qy	303	SGGYDMRNILNGSVQKHPHATVFDNHDSOPGEALESFVQOWFKPLAYALVLTREQ	362
Db	302	QGAEYDMRHIFTGLVEADPFHATLVANHDTPLOALEAPVEPWFKPLAYALVLTREQ	361
Qy	363	YPSVFYGDYGIPTH-----GVPAMKSIDPLLOAROTPAYGTOHDYFDHDI I	411
Db	362	VPSVFYDLYGASYEDSGENGETCRVMPVI-NQJDLILARQFPAHGIQTLFFDHNCI	420
Qy	412	GWTREGNSHPNSGLATIMSDPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGNGN	471
Db	421	AFSRSGTEENP--GCVVVLSNGDDGKTLILLGDVYANKTWEDFSGNRDEYVVVTNDQGEAT	478
Qy	472	PSVNGGVSVMV 483	
Db	479	FFCNAGSVSMV 490	

Search completed: October 7, 2004, 00:20:40  
Job time : 16.886 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.4478 Seconds  
(without alignments)  
2920.093 Million cell updates/sec

Title: US-09-925-576C-2  
Perfect score: 2714  
Sequence: 1 HHNGTNGTMMQYFEWYLPND.....ADGMNFSVNGSVSVWVKQ 485

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2714	100.0	485	9	US-09-769-864-1
2	2714	100.0	485	9	US-09-769-864-7
3	2714	100.0	485	9	US-09-854-346-2
4	2714	100.0	485	9	US-09-902-188A-1
5	2714	100.0	485	9	US-09-918-543-2
6	2714	100.0	485	9	US-09-795-211-1
7	2714	100.0	485	10	US-09-925-576C-2
8	2714	100.0	485	12	US-10-665-667-1
9	2714	100.0	485	12	US-10-665-667-7
10	2714	100.0	485	12	US-10-025-648-1
11	2714	100.0	485	12	US-10-327-837-1
12	2714	100.0	485	12	US-10-327-837-7
13	2714	100.0	485	14	US-10-184-771-12
14	2714	100.0	485	16	US-10-477-725-2
15	2613	96.3	516	9	US-09-986-676A-2

16	2613	96.3	516	9	US-09-971-611-2	Sequence 2, Appli
17	2613	96.3	516	16	US-10-399-161-8	Sequence 8, Appli
18	2456	90.5	516	16	US-10-343-212-2	Sequence 2, Appli
19	2448	90.2	485	9	US-09-769-864-2	Sequence 2, Appli
20	2448	90.2	485	9	US-09-769-864-8	Sequence 8, Appli
21	2448	90.2	485	9	US-09-854-346-4	Sequence 4, Appli
22	2448	90.2	485	9	US-09-902-188A-2	Sequence 2, Appli
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25	2448	90.2	485	10	US-09-925-576C-4	Sequence 4, Appli
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29	2448	90.2	485	12	US-10-327-837-2	Sequence 2, Appli
30	2448	90.2	485	12	US-10-327-837-8	Sequence 8, Appli
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33	2440	89.9	485	9	US-09-854-346-13	Sequence 13, Appli
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36	2440	89.9	485	12	US-10-665-667-6	Sequence 6, Appli
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43	2429	89.5	485	12	US-10-327-837-24	Sequence 24, Appli
44	2429	89.5	485	12	US-10-327-837-26	Sequence 26, Appli
45	2429	89.5	485	14	US-10-209-812-5	Sequence 5, Appli

## ALIGNMENTS

## RESULT 1

US-09-769-864-1  
; Sequence 1, Application US/09769864  
; Patent No. US20010039253A1  
; GENERAL INFORMATION:  
; APPLICANT: Borchert, Torben V.  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Andersen, Carsten  
; APPLICANT: Nielsen, Bjarne  
; APPLICANT: Nissen, Torben L.  
; APPLICANT: Kjaerulff, Soren  
; TITLE OF INVENTION: Alpha-Amulase Mutants  
; FILE REFERENCE: 5368.200-US  
; CURRENT APPLICATION NUMBER: US/09/769,864  
; CURRENT FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/183,412  
; PRIOR FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus  
US-09-769-864-1

Query Match 100.0%; Score 2714; DB 9; Length 485;  
Best Local Similarity 100.0%; Pred. No. 5.3e-241;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 HHNGTNGTMMQYFEWYLPNDGNHNRDRDAANLKSIGITAVWIPPAWKGTQNDVGGA 60

Qy 61 YDLIDLEFNGKGTVRTKYGTNRQLQAATVSLKNGIQVYGVDMNHKGGADGTETINAV 120

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Db 421 HPNSGLATIMSDPGGNKMWYGVKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSYS 480  
Qy 481 VWVKQ 485  
Db 481 VWVKQ 485

RESULT 2  
US-09-769-864-7  
; Sequence 7, Application US/09769864  
; Patent No. US20010039253A1  
; GENERAL INFORMATION:  
; APPLICANT: Borchert, Torben V.  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Andersen, Carsten  
; APPLICANT: Nielsen, Bjarne  
; APPLICANT: Nissen, Torben L.  
; APPLICANT: Kjaerulff, Soren  
; TITLE OF INVENTION: Alpha-Amulase Mutants  
; FILE REFERENCE: 5368.200-US  
; CURRENT APPLICATION NUMBER: US/09/769,864  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-769-864-7

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Best Local Similarity 100.0%; Pred. No. 5.3e-241;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNS 420

Qy 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVDFVPLHYNLNA 300  
Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVDFVPLHYNLNA 300  
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Db 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNS 420  
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Db 421 HPNSGLATIMSDPGGNKMWYGVKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSYS 480  
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Db 481 VWVKQ 485

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; Patent No. US20020068352A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020068352A1ozymes A/S  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Jorgensen, Christel Thea  
; APPLICANT: Nielsen, Bjarne Ronfeldt  
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity  
; FILE REFERENCE: 6140.200-US  
; CURRENT APPLICATION NUMBER: US/09/854,346  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-854-346-2

Query Match 100.0%; Score 2714; DB 9; Length 485;  
Best Local Similarity 100.0%; Pred. No. 5.3e-241;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 YDLYDLGEFNGKQVTRTKYTRNQLQAATVSLKNGIGIYQYGDVVMNHKGADGTEIVNAV 120  
Db 61 YDLYDLGEFNGKQVTRTKYTRNQLQAATVSLKNGIGIYQYGDVVMNHKGADGTEIVNAV 120  
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Db 121 EVNRSNRQETSGEYAEAWTKFDFGRGNHSSFKWRVYHFDGTDQSRQLQNKIYKF 180  
Qy 181 RGTGKAWDEVDTEGNYDYLYADVDMDHPEVHELRLNKGWVYTNLTLDGFRIDAVKH 240  
Db 181 RGTGKAWDEVDTEGNYDYLYADVDMDHPEVHELRLNKGWVYTNLTLDGFRIDAVKH 240  
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Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVDFVPLHYNLNA 300  
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QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480  
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DB 481 VVWKQ 485  
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; Sequence 1, Application US/09795211  
; Publication No. US20020183226A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Kasturi, Chandrika  
; APPLICANT: Wandstrat, Mark E.  
; APPLICANT: Song, Brian X.  
; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZY  
; FILE REFERENCE: Detergent Composition  
; CURRENT APPLICATION NUMBER: US/09/795,211  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: alkaliphilic bacillus  
US-09-795-211-1  
Query Match 100.0%; Score 2714; DB 9; Length 485;  
Best Local Similarity 100.0%; Pred. No. 5.3e-241;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 YDLYLGEFNGKGTVRTKYGTRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
DB 61 YDLYLGEFNGKGTVRTKYGTRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
QY 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
DB 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
QY 181 RGTGKAWDEVDTEGNGYDYLMDVDMDPHPEVHELNRNGVWYTTNLDGFRIDAVKH 240  
DB 181 RGTGKAWDEVDTEGNGYDYLMDVDMDPHPEVHELNRNGVWYTTNLDGFRIDAVKH 240  
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DB 241 IKYSFTRDWLTHVRNTTGKPMFAVABFKNKDLGAIENYLNKTSWNHVSFVDPVPLHNLNA 300  
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DB 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360  
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DB 361 QGYPVFGDYGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420  
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480  
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480  
QY 481 VVWKQ 485

DB 481 VVWKQ 485  
RESULT 7  
US-09-925-576C-2  
; Sequence 2, Application US/09925576C  
; Publication No. US20030129718A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Carsten  
; APPLICANT: Borchert, Torben Vedel  
; APPLICANT: Nielsen, Bjarne Ronfeldt  
; TITLE OF INVENTION: Amylase Variants  
; FILE REFERENCE: 10004.204-US  
; CURRENT APPLICATION NUMBER: US/09/925,576C  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-925-576C-2  
Query Match 100.0%; Score 2714; DB 10; Length 485;  
Best Local Similarity 100.0%; Pred. No. 5.3e-241;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 YDLYLGEFNGKGTVRTKYGTRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
DB 61 YDLYLGEFNGKGTVRTKYGTRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120  
QY 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
DB 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180  
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DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480  
QY 481 VVWKQ 485  
DB 481 VVWKQ 485  
RESULT 8  
US-10-665-667-1  
; Sequence 1, Application US/10665667  
; Publication No. US20040038368A1  
; GENERAL INFORMATION:  
; APPLICANT: Borchert, Torben V.  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Andersen, Carsten

```
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRN
; ORGANISM: Bacillus
US-10-665-667-1

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLYLDFEFNKGKTVRTKYGTRNOLQAAVTSKNGIQQVYGVVNNHKGADGTEIVNAV 120
Db 61 YDLYLDFEFNKGKTVRTKYGTRNOLQAAVTSKNGIQQVYGVVNNHKGADGTEIVNAV 120
Qy 121 EVNRSNRNQETSGEYATEAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYATEAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNYDYLMAVDMDHPEVIELRNWGVWYTNLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLMAVDMDHPEVIELRNWGVWYTNLNDGFRIDAVKH 240
Qy 241 IKYSFTDMLTHVNTTCKPMFAVAEFKNDLGAENLANKTSWNHVSFVQWFKPLAYALVLTRE 300
Db 241 IKYSFTDMLTHVNTTCKPMFAVAEFKNDLGAENLANKTSWNHVSFVQWFKPLAYALVLTRE 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTAVTFVNDHDSQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTAVTFVNDHDSQGEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSVFYGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGGSVS 480
Qy 481 VWVKQ 485
Db 481 VWVKQ 485

RESULT 9
US-10-665-667-7
; Sequence 7, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
```

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; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRN
; ORGANISM: Bacillus sp.
US-10-665-667-7

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLYLDFEFNKGKTVRTKYGTRNOLQAAVTSKNGIQQVYGVVNNHKGADGTEIVNAV 120
Db 61 YDLYLDFEFNKGKTVRTKYGTRNOLQAAVTSKNGIQQVYGVVNNHKGADGTEIVNAV 120
Qy 121 EVNRSNRNQETSGEYATEAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYATEAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNYDYLMAVDMDHPEVIELRNWGVWYTNLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLMAVDMDHPEVIELRNWGVWYTNLNDGFRIDAVKH 240
Qy 241 IKYSFTDMLTHVNTTCKPMFAVAEFKNDLGAENLANKTSWNHVSFVQWFKPLAYALVLTRE 300
Db 241 IKYSFTDMLTHVNTTCKPMFAVAEFKNDLGAENLANKTSWNHVSFVQWFKPLAYALVLTRE 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTAVTFVNDHDSQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTAVTFVNDHDSQGEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSVFYGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGGSVS 480
Qy 481 VWVKQ 485
Db 481 VWVKQ 485

RESULT 10
US-10-025-648-1
; Sequence 1, Application US/10025648
; Publication No. US20030064908A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; Svendsen, Allan
; Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
```

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/025,648
/ FILING DATE: 19-Dec-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/600,656
/ FILING DATE: 13-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lambiris, Elias J.
/ REGISTRATION NUMBER: 33,728
/ REFERENCE/DOCKET NUMBER: 4318.204-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 867 0123
/ TELEFAX: 212 867 0298
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 485 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-025-648-1

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
DB 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAI EAATKFDPFGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYAI EAATKFDPFGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTENGNYDLYMADVDMHPEVIHELNRNGVWYTTNLTLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTENGNYDLYMADVDMHPEVIHELNRNGVWYTTNLTLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLLQARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
DB 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLLQARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
QY 481 VVWVKQ 485
DB 481 VVWVKQ 485

RESULT 11
US-10-327-837-1
; Sequence 1, Application US/10327837
; Publication No. US20030211958A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Svendsen, Allan
/ APPLICANT: Borchert, Torben Vedel
/ APPLICANT: Bisgard-Frantzen Henrik
/ APPLICANT: Outtrup, Helle
/ APPLICANT: Nielsen, Bjarne Ronfeldt
/ APPLICANT: Nielsen, Vibeke Skovgaard
/ APPLICANT: Hoeck, Lisbeth Hedegaard
/ TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
/ FILE REFERENCE: 5276.400-US
/ CURRENT APPLICATION NUMBER: US/10/327,837
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: US/09/290,734
/ PRIOR FILING DATE: 1999-04-13
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 485
/ TYPE: PRT
/ ORGANISM: Bacillus sp.
US-10-327-837-1

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
DB 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAI EAATKFDPFGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYAI EAATKFDPFGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTENGNYDLYMADVDMHPEVIHELNRNGVWYTTNLTLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTENGNYDLYMADVDMHPEVIHELNRNGVWYTTNLTLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLLQARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
DB 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLLQARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
QY 481 VVWVKQ 485
DB 481 VVWVKQ 485

RESULT 12
US-10-327-837-7
; Sequence 7, Application US/10327837
; Publication No. US20030211958A1
/ GENERAL INFORMATION:
/ APPLICANT: Svendsen, Allan
/ APPLICANT: Borchert, Torben Vedel
/ APPLICANT: Bisgard-Frantzen Henrik
/ APPLICANT: Outtrup, Helle
/ APPLICANT: Nielsen, Bjarne Ronfeldt
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; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hosack, Libbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-7

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60

Qy 61 YDLIDLGEFQKQGVTRTKYIGTRNQLQAAVTSKNGIQVYGDVVMNHKGGADGTEIVNAV 120
Db 61 YDLIDLGEFQKQGVTRTKYIGTRNQLQAAVTSKNGIQVYGDVVMNHKGGADGTEIVNAV 120

Qy 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDQDSRQLQNKIKYKF 180
Db 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDQDSRQLQNKIKYKF 180

Qy 181 RGTGKAWDEVDTENGNYDYLMYADVDMHDPEVTHELRNMGVWYTTNTLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTENGNYDYLMYADVDMHDPEVTHELRNMGVWYTTNTLNDGFRIDAVKH 240

Qy 241 IKYSFTDMLTHVNTTGGKPMFAVAEFWQNDLGAENLYNKTSNHVSFVDFPLHNLNA 300
Db 241 IKYSFTDMLTHVNTTGGKPMFAVAEFWQNDLGAENLYNKTSNHVSFVDFPLHNLNA 300

Qy 301 SNSGGYDMENILNGSVVQKHPHATVFDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMENILNGSVVQKHPHATVFDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFYGYGYPITHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYGYGYPITHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420

Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 13
US-10-184-771-12
; Sequence 12, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Biogard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-10-184-771-12

Query Match      100.0%; Score 2714; DB 14; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60

Qy 61 YDLIDLGEFQKQGVTRTKYIGTRNQLQAAVTSKNGIQVYGDVVMNHKGGADGTEIVNAV 120
Db 61 YDLIDLGEFQKQGVTRTKYIGTRNQLQAAVTSKNGIQVYGDVVMNHKGGADGTEIVNAV 120

Qy 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDQDSRQLQNKIKYKF 180
Db 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDQDSRQLQNKIKYKF 180

Qy 181 RGTGKAWDEVDTENGNYDYLMYADVDMHDPEVTHELRNMGVWYTTNTLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTENGNYDYLMYADVDMHDPEVTHELRNMGVWYTTNTLNDGFRIDAVKH 240

Qy 241 IKYSFTDMLTHVNTTGGKPMFAVAEFWQNDLGAENLYNKTSNHVSFVDFPLHNLNA 300
Db 241 IKYSFTDMLTHVNTTGGKPMFAVAEFWQNDLGAENLYNKTSNHVSFVDFPLHNLNA 300

Qy 301 SNSGGYDMENILNGSVVQKHPHATVFDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMENILNGSVVQKHPHATVFDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFYGYGYPITHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYGYGYPITHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420

Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 14
US-10-477-725-2
; Sequence 2, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-477-725-2

Query Match      100.0%; Score 2714; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
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Matches	485;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWI	PPAWKGTSONDVGYGA	60					
Db	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWI	PPAWKGTSONDVGYGA	60					
Qy	61	YDLYDLGFEFNQKGTVRTTKYGTNRQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIVNAV	120						
Db	61	YDLYDLGFEFNQKGTVRTTKYGTNRQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIVNAV	120						
Qy	121	EVNRSNRNQETSGEYAIKAWTKFDPGGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180						
Db	121	EVNRSNRNQETSGEYAIKAWTKFDPGGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180						
Qy	181	RGTKAWDWEVDTENGNYDLYMADVDMDPHPEVIHELNRWGVYVYTNLNLGDFRIDAVKH	240						
Db	181	RGTKAWDWEVDTENGNYDLYMADVDMDPHPEVIHELNRWGVYVYTNLNLGDFRIDAVKH	240						
Qy	241	IKYSFTRDWLTHVRNTTGGKPMFAVAEFWKNDLGAENYLNKTSWNHSPVDPVPLHYNLYNA	300						
Db	241	IKYSFTRDWLTHVRNTTGGKPMFAVAEFWKNDLGAENYLNKTSWNHSPVDPVPLHYNLYNA	300						
Qy	301	SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360						
Db	301	SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360						
Qy	361	QGYPSVFYGYGIPTHGVPAKSKIDPLLOARQTFAYGTOHDYFDHDDIIGWTRGNS	420						
Db	361	QGYPSVFYGYGIPTHGVPAKSKIDPLLOARQTFAYGTOHDYFDHDDIIGWTRGNS	420						
Qy	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFNSVNGGSVS	480						
Db	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFNSVNGGSVS	480						
Qy	481	VWVKQ 485							
Db	481	VWVKQ 485							

RESULT 15  
 US-09-986-676A-2  
 ; Sequence 2, Application US/09986676A  
 ; Patent No. US20020102698A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HATADA, Yuji  
 ; APPLICANT: OZAKI, Katsuya  
 ; APPLICANT: ARA, Katsutoshi  
 ; APPLICANT: KAWAI, Shuji  
 ; APPLICANT: ITO, Susumu  
 ; TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase  
 ; FILE REFERENCE: 2173-0121P  
 ; CURRENT APPLICATION NUMBER: US/09/986.676A  
 ; PRIOR FILING DATE: 2001-11-09  
 ; PRIOR APPLICATION NUMBER: PCT/JP96/01641  
 ; PRIOR FILING DATE: 1996-06-14  
 ; PRIOR APPLICATION NUMBER: Japan 147257/1995  
 ; PRIOR FILING DATE: 1995-06-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 516  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus sp.  
 US-09-986-676A-2

Query Match  
 Best Local Similarity 96.3%; Score 2613; DB 9; Length 516;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWI  
 Db 32 HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWI

Qy	61	YDLYDLGFEFNQKGTVRTTKYGTNRQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIVNAV	120
Db	92	YDLYDLGFEFNQKGTVRTTKYGTNRQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIVNAV	151
Qy	121	EVNRSNRNQETSGEYAIKAWTKFDPGGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180
Db	152	EVNRSNRNQETSGEYTIKAWTKFDPGGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	211
Qy	181	RGTKAWDWEVDTENGNYDLYMADVDMDPHPEVIHELNRWGVYVYTNLNLGDFRIDAVKH	240
Db	212	RGTKAWDWEVDTENGNYDLYMADVDMDPHPEVIHELNRWGVYVYTNLNLGDFRIDAVKH	271
Qy	241	IKYSFTRDWLTHVRNTTGGKPMFAVAEFWKNDLGAENYLNKTSWNHSPVDPVPLHYNLYNA	300
Db	272	IKYSFTRDWLTHVRNTTGGKPMFAVAEFWKNDLGAENYLNKTSWNHSPVDPVPLHYNLYNA	331
Qy	301	SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360
Db	332	SNSGGYDMRNILNGSVVQKHPIHATVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	391
Qy	361	QGYPSVFYGYGIPTHGVPAKSKIDPLLOARQTFAYGTOHDYFDHDDIIGWTRGNS	420
Db	392	QGYPSVFYGYGIPTHGVPSMKSIDPLLOARQTFAYGTOHDYFDHDDIIGWTRGNS	451
Qy	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFNSVNGGSVS	480
Db	452	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRSGTGTVTINADGNGFNSVNGGSVS	511
Qy	481	VWVKQ 485	
Db	512	VWVKQ 516	

Search completed: October 7, 2004, 00:57:24  
 Job time : 55.4478 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.5516 Seconds  
(without alignments)  
2340.424 Million cell updates/sec

Title: US-09-925-576C-4  
Perfect score: 2720  
Sequence: 1 HHNGTNGTMQYFEWHLND.....ADGWANFVNGSVSIWVKR 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_29Jan04.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2720	100.0	485	2 AAR81836	Aar81836 Bacillus
2	2720	100.0	485	2 AAW31500	Aaw31500 Bacillus
3	2720	100.0	485	2 AAW48261	Aaw48261 Bacillus
4	2720	100.0	485	2 AAY15422	Aay15422 Termamyl
5	2720	100.0	485	2 AAY15416	Aay15416 Bacillus
6	2720	100.0	485	2 AAY07382	Aay07382 Wild type
7	2720	100.0	485	3 AAY99609	Aay99609 Bacillus
8	2720	100.0	485	3 AAY99603	Aay99603 Bacillus
9	2720	100.0	485	5 ABB06934	Abb06934 Bacillus
10	2720	100.0	485	5 AAU12150	Aau12150 Bacillus
11	2720	100.0	485	5 AAB47851	Aab47851 Bacillus
12	2720	100.0	485	5 ABB76587	Abb76587 Termamyl
13	2720	100.0	485	6 ABB99481	Abb99481 Amino aci
14	2720	100.0	834	4 AAB30701	Aab30701 A Bacillu
15	2712	99.7	485	2 AAY07392	Aay07392 Wild type
16	2709	99.6	485	5 ABB76636	Abb76636 Termamyl
17	2708	99.6	485	5 ABB76639	Abb76639 Termamyl
18	2707	99.5	485	2 AAY25151	Aay25151 Bacillus
19	2706	99.5	485	5 ABB76637	Abb76637 Termamyl
20	2705	99.4	485	5 ABB76643	Abb76643 Termamyl
21	2703	99.4	485	5 ABB76640	Abb76640 Termamyl
22	2701	99.3	485	5 ABB76644	Abb76644 Termamyl
23	2701	99.3	485	5 ABB76641	Abb76641 Termamyl
24	2701	99.3	485	5 ABB76642	Abb76642 Termamyl
25	2698	99.2	483	2 AAW12139	Aaw12139 Alpha-amy

26	2698	99.2	485	5 ABB76638	Abb76638 Termamyl
27	2697	99.2	483	2 AAW12137	Aaw12137 Alpha-amy
28	2697	99.2	483	2 AAY13444	Aay13444 Alpha-amy
29	2692	99.0	481	4 ABBM0011	Abbm0011 Bacillus
30	2691	98.9	483	2 AAW12138	Aaw12138 Alpha-amy
31	2691	98.9	483	2 AAW12140	Aaw12140 Alpha-amy
32	2690	98.9	483	2 AAW12143	Aaw12143 Alpha-amy
33	2457	90.3	485	2 AAW12110	Aaw12110 Alpha-amy
34	2455	90.3	485	2 AAW12144	Aaw12144 Alpha-amy
35	2454	90.2	485	2 AAW12109	Aaw12109 Alpha-amy
36	2448	90.0	485	2 AAW31499	Aaw31499 Bacillus
37	2448	90.0	485	2 AAW48260	Aaw48260 Bacillus
38	2448	90.0	485	2 AAY15421	Aay15421 Termamyl
39	2448	90.0	485	2 AAY15415	Aay15415 Bacillus
40	2448	90.0	485	2 AAY25150	Aay25150 Bacillus
41	2448	90.0	485	2 AAY07391	Aay07391 Wild type
42	2448	90.0	485	2 AAY07381	Aay07381 Wild type
43	2448	90.0	485	3 AAY99602	Aay99602 Bacillus
44	2448	90.0	485	3 AAY99608	Aay99608 Bacillus
45	2448	90.0	485	5 ABB06933	Abb06933 Bacillus

## ALIGNMENTS

### RESULT 1

AAR81836  
ID AAR81836 standard; protein; 485 AA.  
XX AAR81836;  
XX  
DT 16-MAR-1996 (first entry)  
XX  
DE Bacillus sp. alkaline alpha-amylase.  
XX  
KW Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile; beer;  
KW starch.  
XX  
OS Bacillus.  
XX  
FN W09526397-A1.  
XX  
PD 05-OCT-1995.  
XX  
PF 29-MAR-1995; 95WO-DK000142.  
XX  
PR 29-MAR-1994; 94DK-00000353.  
PR 03-NOV-1994; 94DK-00001271.  
PR 03-FEB-1995; 95DK-00000123.  
(NOVO ) NOVO-NORDISK AS.

Outtrup H, Bisgard-Frantzen H, Ostergaard PR, Rasmussen MD;  
Van Der Zee P;

WPI; 1995-351318/45.  
N-PSDB; AAT00777.

New alkaline Bacillus alpha-amylase - used in e.g. detergent compans.  
starch liquefaction, textile desizing, starch modification or beer  
making.

Claim 5; Page 46-48; 65pp; English.

This alpha-amylase protein is characterized by having a specific activity  
at least 25% higher than the specific activity of Termamyl at 25-55 deg C  
and a pH of 8-10. The enzyme can be used in detergent composition for  
starch liquefaction, the production of lignocellulosic materials, e.g.  
pulp, paper and cardboard from waste containing starch, for deinking  
recycled starch-coated, or starch- containing printed paper, to modify  
starch for papermaking, for textile desizing, and beer-making processes.  
This protein may be produced recombinantly

SQ	Sequence 485 AA;	
PT	Query Match	100.0%; Score 2720; DB 2; Length 485;
PT	Best Local Similarity	100.0%; Pred. No. 3.2e-212; Indels 0; Gaps 0;
XX	Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PS	Claim 1; Page 88-89; 97pp; English.	
XX	The present sequence is a Bacillus sp. alpha amylase with a specific activity at least 25% higher than that of Termamyl (RTM) at 25 to 55 degrees C at pH 8 to 10, measured by the Phadebas (RTM) activity test. It is of use in hard surface cleaning, hand or machine dishwashing and laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain removal and fabric care are obtained by using it at a concentration of 0.00018 to 0.06%	
XX	Sequence 485 AA;	
SQ	Query Match	100.0%; Score 2720; DB 2; Length 485;
SQ	Best Local Similarity	100.0%; Pred. No. 3.2e-212; Indels 0; Gaps 0;
SQ	Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 HNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRGITAIWIPPAWKTSQNDVGYGA 60	
DB	1 HNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRGITAIWIPPAWKTSQNDVGYGA 60	
QY	61 YDLYLGEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVYGVVMMHKGADATENVLAV 120	
DB	61 YDLYLGEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVYGVVMMHKGADATENVLAV 120	
QY	121 EVNPNRNRQIEISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVWDQSRQFNRIYKF 180	
DB	121 EVNPNRNRQIEISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVWDQSRQFNRIYKF 180	
QY	181 RGDGKAWDEVDSENGNYDILMYADVMDHPVNNELRWGEWYTTNLNDGFRIDAVKH 240	
DB	181 RGDGKAWDEVDSENGNYDILMYADVMDHPVNNELRWGEWYTTNLNDGFRIDAVKH 240	
QY	241 IKYSFTRDMLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDPVPLHYNLYNA 300	
DB	241 IKYSFTRDMLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDPVPLHYNLYNA 300	
QY	301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPQGESLESFVQEWFKELAYALILTRE 360	
DB	301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPQGESLESFVQEWFKELAYALILTRE 360	
QY	361 QGYPSVFYGDYIGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420	
DB	361 QGYPSVFYGDYIGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420	
QY	421 HPNSGLATIMSDPGGKEMWYGVQNKAGQVWHDIITGNKPGTGTINADGWANFVNGSGVS 480	
DB	421 HPNSGLATIMSDPGGKEMWYGVQNKAGQVWHDIITGNKPGTGTINADGWANFVNGSGVS 480	
QY	481 IWVKR 485	
DB	481 IWVKR 485	
RESULT 3		
AAW48261		
ID	AAW48261 standard; protein; 485 AA.	
XX		
AC	AAW48261;	
DT	02-JUL-1998 (first entry)	
XX		
DE	Bacillus sp. alpha amylase protein #2.	
XX		
KW	Alpha amylase; stain digestion; detergent; fabric laundry performance.	
XX		
OS	Bacillus sp.	
XX		
PN	WO9805748-A1.	
XX		
PD	12-FEB-1998.	

XX 01-AUG-1996; 96WO-US012612.  
XX 01-AUG-1996; 96WO-US012612.  
XX (PROC ) PROCTER & GAMBLE CO.  
XX Baek AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;  
XX WPI; 1998-159168/14.  
XX Use of specific alpha-amylase enzymes - in laundry detergent compositions  
XX to provide effective cleaning and whitening of dingy fabrics.  
XX Claim 1; Page 71-72; 82pp; English.  
XX This sequence represents an alpha amylase from Bacillus sp. which is used  
XX in a laundry detergent. The detergent compositions can be used for  
XX boosting fabric laundry performance or for dingy fabric cleanup  
XX  
SQ Sequence 485 AA;  
Query Match 100.0%; Score 2720; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 3.2e-212;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60  
DB 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60  
QY 61 YDLYDLGEFQKGTVRTKYGRSQAIAHALKNGVQVYGVVNMHKGADATENVLAV 120  
DB 61 YDLYDLGEFQKGTVRTKYGRSQAIAHALKNGVQVYGVVNMHKGADATENVLAV 120  
QY 121 EVNPNRNRQISGDTTIEAWTKPFGKNTYSDFKRWYHFGVDVQSRQFQNRYYKF 180  
DB 121 EVNPNRNRQISGDTTIEAWTKPFGKNTYSDFKRWYHFGVDVQSRQFQNRYYKF 180  
QY 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRNGEWTNTNLDDGFRIDAVKH 240  
DB 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRNGEWTNTNLDDGFRIDAVKH 240  
QY 241 IKYSFTRDLWLTNRNATGKEMFAVAEFKNDLGALENLNTNNHNSVDFVPLHNLNA 300  
DB 241 IKYSFTRDLWLTNRNATGKEMFAVAEFKNDLGALENLNTNNHNSVDFVPLHNLNA 300  
QY 301 SNSGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPGESLESFVQEWFKPLAYALILTRE 360  
DB 301 SNSGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPGESLESFVQEWFKPLAYALILTRE 360  
QY 361 QGYPSVFYGYGIPTHSVPAKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRGNTT 420  
DB 361 QGYPSVFYGYGIPTHSVPAKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRGNTT 420  
QY 481 IWVKR 485  
DB 481 IWVKR 485  
RESULT 4  
AA15422  
ID AAY15422 standard; protein; 485 AA.  
XX AC  
XX AAY15422;  
XX AC  
XX 22-JUL-1999 (first entry)  
XX DE  
XX Termamyl-like alpha-amylase protein.

Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;  
sweetener; ethanol; starch; textile desizing; starch liquefaction;  
saccharification process.  
Bacillus sp.  
WO99232211-A1.  
14-MAY-1999.  
30-OCT-1998; 98WO-DK000471.  
30-OCT-1997; 97DK-00001240.  
14-JUL-1998; 98DK-00000936.  
(NOVO ) NOVO-NORDISK AS.  
Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;  
Kjaerulff S;  
WPI; 1999-326987/27.  
New Termamyl-like alpha-amylase variants.  
Claim 38; Page 89-91; 115pp; English.  
The specification describes termamyl-like alpha-amylase variants that  
have altered amino acid sequences to improve properties. The variants are  
produced by creating one or more of the following mutations in amino acid  
sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,  
D144, F145, P146, G147, D148, G149, Q174, R181, G182, D183, G184, K185,  
A186, W189, N195, H107, K108, G109, D166, W167, D168, Q169, S170,  
R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,  
K311, E346, K385, G456, N457, K458, G460, T461, V462, T463. The  
variants can be used for washing and/or dishwashing. They can also be  
used in the production of sweeteners and ethanol from starch, and/or for  
textile desizing, and in starch liquefaction and/or saccharification  
processes. The present amylase can function as the parent sequence in the  
production of the variants of the invention  
SQ Sequence 485 AA;  
Query Match 100.0%; Score 2720; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 3.2e-212;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60  
DB 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60  
QY 61 YDLYDLGEFQKGTVRTKYGRSQAIAHALKNGVQVYGVVNMHKGADATENVLAV 120  
DB 61 YDLYDLGEFQKGTVRTKYGRSQAIAHALKNGVQVYGVVNMHKGADATENVLAV 120  
QY 121 EVNPNRNRQISGDTTIEAWTKPFGKNTYSDFKRWYHFGVDVQSRQFQNRYYKF 180  
DB 121 EVNPNRNRQISGDTTIEAWTKPFGKNTYSDFKRWYHFGVDVQSRQFQNRYYKF 180  
QY 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRNGEWTNTNLDDGFRIDAVKH 240  
DB 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRNGEWTNTNLDDGFRIDAVKH 240  
QY 241 IKYSFTRDLWLTNRNATGKEMFAVAEFKNDLGALENLNTNNHNSVDFVPLHNLNA 300  
DB 241 IKYSFTRDLWLTNRNATGKEMFAVAEFKNDLGALENLNTNNHNSVDFVPLHNLNA 300  
QY 301 SNSGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPGESLESFVQEWFKPLAYALILTRE 360  
DB 301 SNSGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPGESLESFVQEWFKPLAYALILTRE 360  
QY 361 QGYPSVFYGYGIPTHSVPAKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRGNTT 420  
DB 361 QGYPSVFYGYGIPTHSVPAKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRGNTT 420

QY 421 HNSGLATIMSDGPGGKMYVGNKAGQVWHDITGNKPGTIVTINADGWANFVNGGSVS 480  
DB 421 HNSGLATIMSDGPGGKMYVGNKAGQVWHDITGNKPGTIVTINADGWANFVNGGSVS 480

QY 481 IWVKR 485  
DB 481 IWVKR 485

RESULT 5  
ID AAY15416 standard; protein; 485 AA.  
AC AAY15416;  
XX  
DT 22-JUL-1999 (first entry)  
XX  
DE Bacillus alpha-amylase protein.  
XX  
KW Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;  
KW sweetener; ethanol; starch; textile desizing; starch liquefaction;  
KW saccharification process.  
XX  
OS Bacillus sp.  
XX  
XX WO9923211-A1.  
XX  
PD 14-MAY-1999.  
XX  
XX 30-OCT-1998; 98WO-DK000471.  
PF  
PR 30-OCT-1997; 97DK-00001240.  
PR 14-JUL-1998; 98DK-0000936.  
XX  
XX (NOVO ) NOVO-NORDISK AS.  
PA  
XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;  
PI Kjaerulff S;  
XX  
XX WPI; 1999-326987/27.  
DR  
XX  
PT  
XX  
PS  
XX  
CC The specification describes termamyl-like alpha-amylase variants that  
CC have altered amino acid sequences to improve properties. The variants are  
CC produced by creating one or more of the following mutations in amino acid  
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,  
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,  
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,  
CC L171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,  
CC K311, E346, K385, G456, K457, K458, N459, G460, T461, V462, T463. The  
CC variants can be used for washing and/or dishwashing. They can also be  
CC used in the production of sweeteners and ethanol from starch, and/or for  
CC textile desizing, and in starch liquefaction and/or saccharification  
CC processes. The present amylase can function as the parent sequence in the  
CC production of the variants of the invention  
XX  
SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 3.2e-212;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPNQDNHNRRLRDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60  
DB 1 HNGTNGTMMQYFEWHLPNQDNHNRRLRDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60

QY 61 YDLYDLGEFNKQGTVRTKYGTRSOLESIAIHALKNNGVQVYGDVVMNHKGGADATENVLAV 120  
DB 61 YDLYDLGEFNKQGTVRTKYGTRSOLESIAIHALKNNGVQVYGDVVMNHKGGADATENVLAV 120

QY 121 EVNPNRNOBISGDTTIEAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSQRFQNRYYKF 180  
DB 121 EVNPNRNOBISGDTTIEAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSQRFQNRYYKF 180

QY 181 RGDGKAWDEVDSENGNNDYLYMAYADVMDHPHPEVNVNLRWGEWYTTNLNDGFRIDAVKH 240  
DB 181 RGDGKAWDEVDSENGNNDYLYMAYADVMDHPHPEVNVNLRWGEWYTTNLNDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENYLKTNWHSVFDVPLHYNLYNA 300  
DB 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENYLKTNWHSVFDVPLHYNLYNA 300

QY 301 SNSGGNYDMAKLNGTVVQKHPMHAVTFVDNHDSDQFSGESLEFVQWFKPLAYALILTRE 360  
DB 301 SNSGGNYDMAKLNGTVVQKHPMHAVTFVDNHDSDQFSGESLEFVQWFKPLAYALILTRE 360

QY 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILARPONFAYGTQHDYFDHNNIIGWTREGNTT 420  
DB 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILARPONFAYGTQHDYFDHNNIIGWTREGNTT 420

QY 421 HNSGLATIMSDGPGGKMYVGNKAGQVWHDITGNKPGTIVTINADGWANFVNGGSVS 480  
DB 421 HNSGLATIMSDGPGGKMYVGNKAGQVWHDITGNKPGTIVTINADGWANFVNGGSVS 480

QY 481 IWVKR 485  
DB 481 IWVKR 485

RESULT 6  
ID AAY07382 standard; protein; 485 AA.  
XX  
AC AAY07382;  
XX  
DT 16-JUL-1999 (first entry)  
XX  
DE Wild type Termamyl(RTM)-like alpha-amylase protein #2.  
XX  
KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;  
KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;  
KW ethanol.  
XX  
OS Bacillus sp.  
XX  
PH Key Location/Qualifiers  
FT Misc-difference 181..184  
FT /note= "optionally 1, 2, 3 or all residues are deleted"  
FT Misc-difference 195  
FT /note= "optionally altered to any amino acid except an  
FT Asn residue"  
FT Misc-difference 206  
FT /note= "optionally altered to any amino acid except a Val  
FT residue"  
FT Misc-difference 212  
FT /note= "optionally altered to any amino acid except a Glu  
FT residue"  
FT Misc-difference 216  
FT /note= "optionally altered to any amino acid except a Glu  
FT residue"  
FT Misc-difference 269  
FT /note= "optionally altered to any amino acid except a Lys  
FT residue"  
XX  
XX WO9919467-A1.  
XX  
XX 22-APR-1999.  
XX  
XX 13-OCT-1998; 98WO-DK000444.  
XX  
XX 13-OCT-1997; 97DK-00001172.  
XX

PA (NOVO ) NOVO-NORDISK AS.  
XX KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;  
XX KW saccharification; mutein; mutant; enzyme stability; hybrid.  
XX OS Bacillus sp.  
XX FN WO200029560-A1.  
XX PD 25-MAY-2000.  
XX PF 16-NOV-1999; 99WO-DK000628.  
XX PR 16-NOV-1998; 98DK-00001495.  
XX PA (NOVO ) NOVO-NORDISK AS.  
XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;  
XX DR WPI; 2000-387777/33.  
XX PT Variant of parent termamyl-like alpha amylase useful for washing, textile  
XX PT desizing and starch liquefaction, comprising alterations in one or more  
XX PT solvent exposed amino acid residues.  
XX FS Claim 8; Page 64-65; 80pp; English.  
XX CC The present sequence is a parent alpha-amylase from which mutants with  
XX CC increased stability at acidic pH, low calcium concentration and high  
XX CC temperatures have been derived. The sequence encoding this enzyme was  
XX CC isolated from a Bacillus genomic DNA library. A variant may contain  
XX CC mutations in one or more solvent exposed amino acid residues to increase  
XX CC the overall hydrophobicity of the enzyme or the overall number of methyl  
XX CC groups in the side chains of exposed residues may be increased. The  
XX CC mutations can be incorporated by site-directed mutagenesis or by random  
XX CC mutagenesis. As a result of their increased stability, the variants are  
XX CC suitable for the industrial processing of starch, i.e. starch  
XX CC liquefaction and saccharification. They may also be useful for washing,  
XX CC dishwashing and textile desizing. Hybrid alpha-amylases comprising  
XX CC partial amino acid sequences derived from two or more alpha-amylases have  
XX CC also been created in order to increase enzyme stability  
XX SQ Sequence 485 AA;  
Query Match 100.0%; Score 2720; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 3.2e-212;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HHNGTGTMMQYFEWHLFNDGNHWNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60  
DB 1 HHNGTGTMMQYFEWHLFNDGNHWNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60  
QY 61 YDLYDLGFEFQKQGVTRTKYGRSQAIAHAKKNGVQVYGDVVMNHKGGADATENVLAV 120  
DB 61 YDLYDLGFEFQKQGVTRTKYGRSQAIAHAKKNGVQVYGDVVMNHKGGADATENVLAV 120  
QY 121 EVNPNRNRQISGDTTTEAWTKDFPGRGNTYSDFKRWYHFDGVDWQDSQFQNRKYKF 180  
DB 121 EVNPNRNRQISGDTTTEAWTKDFPGRGNTYSDFKRWYHFDGVDWQDSQFQNRKYKF 180  
QY 181 RGDGKAWDWEVDSENGNYDYLMAVDMDHPEVNNELRWGEWYTNLNDGFRIDAVKH 240  
DB 181 RGDGKAWDWEVDSENGNYDYLMAVDMDHPEVNNELRWGEWYTNLNDGFRIDAVKH 240  
QY 241 IKYSFTEDLWTHVRNATGKEMFAVAEFWKNDLGALENLKNKNHSHVDFVPLHYNLYNA 300  
DB 241 IKYSFTEDLWTHVRNATGKEMFAVAEFWKNDLGALENLKNKNHSHVDFVPLHYNLYNA 300  
QY 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
DB 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
QY 361 QGYPVSFYGDYIGTPHSHVPAMKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420  
DB 361 QGYPVSFYGDYIGTPHSHVPAMKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420  
QY 421 HPNSGLATIMSDGPGGKMWYVQNKAGQVWHDDITGNKPGVTNTNADGNWFSVNGGSVS 480  
DB 421 HPNSGLATIMSDGPGGKMWYVQNKAGQVWHDDITGNKPGVTNTNADGNWFSVNGGSVS 480  
QY 481 IWVKR 485  
DB 481 IWVKR 485  
RESULT 7  
ID AAY99609  
AC AAY99609 standard; protein; 485 AA.  
XX AAY99609;  
XX 04-SEP-2000 (first entry)  
XX Bacillus Termamyl-like alpha-amylase #4.

Db 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
 QY 421 HNSGLATTMSDGPGEKMYVQNKAGOVHDDITGNKPGTVTINADGWANFVNGGSYS 480  
 Db 421 HNSGLATTMSDGPGEKMYVQNKAGOVHDDITGNKPGTVTINADGWANFVNGGSYS 480  
 QY 481 IWVKR 485  
 Db 481 IWVKR 485

RESULT 8  
 AAY99603  
 ID AAY99603 standard; protein; 485 AA.  
 AC AAY99603;  
 XX  
 XX  
 DT 04-SEP-2000 (first entry)  
 DE Bacillus parent Termamyl-like alpha-amylase #2.  
 XX  
 XX  
 KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;  
 KW saccharification; mutein; mutant; enzyme stability; hybrid.  
 XX  
 OS Bacillus sp.  
 XX  
 XX WO200029560-A1.  
 PN  
 XX  
 XX 25-MAY-2000.  
 XX  
 PF 16-NOV-1999; 99WO-DR000628.  
 XX  
 PR 16-NOV-1998; 98DK-00001495.  
 XX  
 XX (NOVO ) NOVO-NORDISK AS.  
 PA  
 XX  
 PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;  
 XX  
 DR WPI: 2000-38777/33.  
 DR N-PSDB; AAA48482.  
 XX  
 XX Variant of parent termamyl-like alpha amylase useful for washing, textile  
 PT desizing and starch liquefaction, comprising alterations in one or more  
 PT solvent exposed amino acid residues.  
 XX  
 XX Claim 8; Page 54-56; 80pp; English.  
 XX  
 XX The present sequence is a parent Termamyl-like alpha-amylase from which  
 CC mutants with increased stability at acidic pH, low calcium concentration  
 CC and high temperatures have been derived. The sequence encoding this  
 CC enzyme was isolated from a Bacillus genomic DNA library. A variant may  
 CC contain mutations in one or more solvent exposed amino acid residues to  
 CC increase the overall hydrophobicity of the enzyme or the overall number  
 CC of methyl groups in the side chains of exposed residues may be increased.  
 CC The mutations can be incorporated by site-directed mutagenesis or by  
 CC random mutagenesis. As a result of their increased stability, the  
 CC variants are suitable for the industrial processing of starch, i.e.  
 CC starch liquefaction and saccharification. They may also be useful for  
 CC washing, dishwashing and textile desizing. Hybrid alpha-amylases  
 CC comprising partial amino acid sequences derived from two or more alpha-  
 CC amylases have also been created in order to increase enzyme stability  
 XX  
 XX Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 3; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPDNGNHNRLRDDASLNRRNGITAIWIPPAWKGTQNDVGYGA 60  
 Db 1 HNGTNGTMMQYFEWHLPDNGNHNRLRDDASLNRRNGITAIWIPPAWKGTQNDVGYGA 60  
 QY 61 YDLYLGEFNGKGTVRTKYSQLESIAHALKNNGVQYVGVMMHKGADATENVLAV 120

Db 61 YDLYLGEFNGKGTVRTKYSQLESIAHALKNNGVQYVGVMMHKGADATENVLAV 120  
 QY 121 EVNPNRNQIEISGDYITIAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSQRFQNRYYKF 180  
 Db 121 EVNPNRNQIEISGDYITIAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSQRFQNRYYKF 180  
 QY 181 RGDGKAWDEVDSENGNYDYLAVDMDHPPEVNNELRWGSEWYNTNLDGFRIDAVKH 240  
 Db 181 RGDGKAWDEVDSENGNYDYLAVDMDHPPEVNNELRWGSEWYNTNLDGFRIDAVKH 240  
 QY 241 IKYSFTTRDLTHVRNATGKEMFAVEFWKNDLGALENYLNKTNWNSHSDVPLHYNLXNA 300  
 Db 241 IKYSFTTRDLTHVRNATGKEMFAVEFWKNDLGALENYLNKTNWNSHSDVPLHYNLXNA 300  
 QY 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSDPGESLESFVQWFKPLAYALITRE 360  
 Db 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSDPGESLESFVQWFKPLAYALITRE 360  
 QY 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
 Db 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
 QY 421 HNSGLATTMSDGPGEKMYVQNKAGOVHDDITGNKPGTVTINADGWANFVNGGSYS 480  
 Db 421 HNSGLATTMSDGPGEKMYVQNKAGOVHDDITGNKPGTVTINADGWANFVNGGSYS 480  
 QY 481 IWVKR 485  
 Db 481 IWVKR 485

RESULT 9  
 ABB06934  
 ID ABB06934 standard; protein; 485 AA.  
 XX  
 AC ABB06934;  
 XX  
 DT 19-JUN-2002 (first entry)  
 XX  
 DE Bacillus termamyl-like alpha-amylase protein SEQ ID NO:4.  
 XX  
 XX Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;  
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;  
 KW washing; sweetener; ethanol; starch.  
 XX  
 OS Bacillus sp.  
 XX  
 XX WO200166712-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 07-MAR-2001; 2001WO-DK000144.  
 XX  
 PR 08-MAR-2000; 2000DK-00000376.  
 PR 15-MAR-2000; 2000US-0189857P.  
 PR 23-FEB-2001; 2001DK-0000303.  
 PR 26-FEB-2001; 2001US-0271382P.  
 XX  
 XX (NOVO ) NOVOZYMES AS.  
 PA  
 XX  
 XX Andersen C, Borchert TV, Nielsen BR;  
 PI  
 XX  
 XX WPI; 2002-239612/29.  
 DR N-PSDB; ABL50565.  
 XX  
 XX Novel variant of parent termamyl-like alpha-amylase useful as a component  
 PT in washing and dishwashing compositions, for textile desizing, for starch  
 PT liquefaction, and for producing sweeteners and ethanol from starch.  
 XX  
 PS Claim 8; Page 135-136; 153pp; English.  
 XX  
 XX The present invention describes a variant of a parent termamyl-like alpha

CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more  
 CC positions of a group of 31 possible amino acid positions. The alteration  
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,  
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,  
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,  
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for  
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.  
 CC (I) is useful as a component in hard surface cleaning detergent  
 CC composition, and for producing sweeteners and ethanol from starch. (I)  
 CC has altered solubility, preferably increased solubility, in particular  
 CC under washing, dish washing or hard surface cleaning conditions. The  
 CC present sequence represents a *Bacillus* termamyl-like alpha-amylase which  
 CC is used in the exemplification of the present invention

XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 5; Length 485;

Best Local Similarity 100.0%; Pred. No. 3.2e-212; Mismatches 0; Indels 0; Gaps 0;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWHLPDNDGNHNRRLDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60  
 DB 1 HNGTGTMMQYFEWHLPDNDGNHNRRLDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60  
 QY 61 YDLYDLGEFQKGTVRTKYTRSQLESIAHALKNGVQVYGVVNMHKGADATENVLAV 120  
 DB 61 YDLYDLGEFQKGTVRTKYTRSQLESIAHALKNGVQVYGVVNMHKGADATENVLAV 120  
 QY 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKWRWYHFDGVDMQDQSRQFNRIYKF 180  
 DB 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKWRWYHFDGVDMQDQSRQFNRIYKF 180  
 QY 181 RGDGKAWDEVDSENGNYDLYMADVMDHPVNVNLRNGEWTNTLNDGFRIDAVKH 240  
 DB 181 RGDGKAWDEVDSENGNYDLYMADVMDHPVNVNLRNGEWTNTLNDGFRIDAVKH 240  
 QY 241 IKYSFTRDWLTHVRNATGKEMFAVAEFKNDLGALENYLNKTNWHSVFDVPLHNLNYA 300  
 DB 241 IKYSFTRDWLTHVRNATGKEMFAVAEFKNDLGALENYLNKTNWHSVFDVPLHNLNYA 300  
 QY 301 SNSSGNYDMAKLNGTIVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360  
 DB 301 SNSSGNYDMAKLNGTIVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360  
 QY 361 QGYPSVFGYGYGIPHTSHVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRENTT 420  
 DB 361 QGYPSVFGYGYGIPHTSHVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRENTT 420  
 QY 421 HPNSGLATINSDGPGGKMWYVGNKAGQVWHDTITGNKPGTIVTINADGWANFVSNGGSVS 480  
 DB 421 HPNSGLATINSDGPGGKMWYVGNKAGQVWHDTITGNKPGTIVTINADGWANFVSNGGSVS 480  
 QY 481 IWVKR 485  
 DB 481 IWVKR 485

RESULT 10

AAU12150

ID AAU12150 standard; protein; 485 AA.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

PN W0200188107-A2.

XX 22-NOV-2001.

XX 10-MAY-2001; 2001WO-DK000323.

XX 12-MAY-2000; 2000DK-00000779.

XX (NOVO ) NOVOZYMES AS.

PA Svendsen A, Jorgensen CT, Nielsen BR;

PI WPI; 2002-106123/14.

XX N-PSDB; AAS20023.

XX New variant of parent Termamyl-like alpha-amylase for use as a component

XX in washing and dishwashing compositions, for textile desizing, for starch

XX liquefaction, and for producing sweeteners and ethanol from starch.

XX Claim 5; Fig 1; 84pp; English.

XX The invention relates to a variant of parent TERMAMYL-like alpha- amylase

XX comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,

XX or at position 234, where the variant has alpha-amylase activity and each

XX position corresponds to a position of a parent termamyl-like alpha-

XX amylase sequence having a *Bacillus* licheniformis alpha-amylase sequence

XX of 483 amino acids, given in specification. The variant alpha- amylase, a

XX detergent additive comprising the variant or a detergent composition

XX comprising the variant, is useful for washing and/or dishwashing or

XX textile desizing. The alpha-amylase is useful for starch liquefaction or

XX ethanol production and as a component in a hard surface cleaning

XX detergent composition, and for producing sweeteners from starch. The

XX variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage

XX activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic

XX branch linkage cleavage activity of amylopectin or a limit dextrin

XX prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a

XX natural variant of the TERMAMYL alpha-amylase, SP722

XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 5; Length 485;

Best Local Similarity 100.0%; Pred. No. 3.2e-212;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWHLPDNDGNHNRRLDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60

DB 1 HNGTGTMMQYFEWHLPDNDGNHNRRLDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60

QY 61 YDLYDLGEFQKGTVRTKYTRSQLESIAHALKNGVQVYGVVNMHKGADATENVLAV 120

DB 61 YDLYDLGEFQKGTVRTKYTRSQLESIAHALKNGVQVYGVVNMHKGADATENVLAV 120

QY 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKWRWYHFDGVDMQDQSRQFNRIYKF 180

DB 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKWRWYHFDGVDMQDQSRQFNRIYKF 180

QY 181 RGDGKAWDEVDSENGNYDLYMADVMDHPVNVNLRNGEWTNTLNDGFRIDAVKH 240

DB 181 RGDGKAWDEVDSENGNYDLYMADVMDHPVNVNLRNGEWTNTLNDGFRIDAVKH 240

QY 241 IKYSFTRDWLTHVRNATGKEMFAVAEFKNDLGALENYLNKTNWHSVFDVPLHNLNYA 300

DB 241 IKYSFTRDWLTHVRNATGKEMFAVAEFKNDLGALENYLNKTNWHSVFDVPLHNLNYA 300

QY 301 SNSSGNYDMAKLNGTIVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360

DB 301 SNSSGNYDMAKLNGTIVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360

QY 361 QGYPSVFGYGYGIPHTSHVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRENTT 420

DB 361 QGYPSVFGYGYGIPHTSHVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRENTT 420

QY 421 HPNSGLATINSDGPGGKMWYVGNKAGQVWHDTITGNKPGTIVTINADGWANFVSNGGSVS 480

DB 421 HPNSGLATINSDGPGGKMWYVGNKAGQVWHDTITGNKPGTIVTINADGWANFVSNGGSVS 480

QY 481 IWVKR 485

DB 481 IWVKR 485

Db 421 HPSGLATIMSDGPGGKMYVGQKAGQVWHDTGNKPGTGTINADGWANFVNGGSVS 480  
QY 481 IWVKR 485  
Db 481 IWVKR 485  
RESULT 11  
AAB47851  
ID AAB47851 standard; protein; 485 AA.  
XX AAB47851;  
XX 02-APR-2002 (first entry)  
XX Bacillus alpha amylase sp722.  
XX Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;  
KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;  
KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;  
KW cured meat; fermented meat; spice.  
XX Bacillus sp.  
XX WO200196537-A2.  
XX 20-DEC-2001.  
XX 13-JUN-2001; 2001WO-DK00404.  
XX 14-JUN-2000; 2000DK-00000917.  
XX 20-JUN-2000; 2000US-0212852P.  
XX (NOVO ) NOVOZYMES AS.  
XX Nielsen BR, Weibye M;  
XX WPI; 2002-098064/13.  
XX N-PSDB; AAI72212.  
XX New modified alpha-amylase derived from the genus Bacillus and/or is a  
PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing  
PT maltodextrin or glucose syrup.  
XX Claim 5; Page 28-30; 47pp; English.  
XX The sequences given in AAB47850-56 show modified alpha-amylases derived  
CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-  
CC amylase and they have been pre-oxidized. The alpha amylase is useful for  
CC producing a maltodextrin or glucose syrup, by treating starch with a pre-  
CC oxidized alpha-amylase until a product with a DE between 5-45 has been  
CC provided and/or until a product with a molecular weight of between 5-30  
CC kDa has been provided. The product comprises a maltodextrin with a DE of  
CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The  
CC alpha amylase is useful for producing a maltodextrin or glucose syrup,  
CC where the glucose syrup is useful as an ingredient in food, feed or  
CC pharmaceuticals. Glucose syrup is useful in confectionery such as  
CC candies, beverages such as isotonic drinks, bakery such as cereal bars,  
CC dairy and ice cream such as coffee whiteners, conventional foods such as  
CC salad dressings, and food ingredients and preparations such as cured  
CC meat, fermented meat, spices and seasoning encapsulated flavours  
XX Sequence 485 AA;  
SQ Query Match 100.0%; Score 2720; DB 5; Length 485;  
Best Local Similarity 100.0%; Pred. No. 3.2e-212;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HNGTGTMMQYFEWHLPGNDGNHNRDRDASLNRNGITAIWIPPAWKGTSDNDVGGA 60  
Db 1 HNGTGTMMQYFEWHLPGNDGNHNRDRDASLNRNGITAIWIPPAWKGTSDNDVGGA 60

QY 61 YDLYDLGEFNOKGTVRTKYGTRSQLESATHALKNGGVQVYGDVVMNHKGGADATENVLAY 120  
Db 61 YDLYDLGEFNOKGTVRTKYGTRSQLESATHALKNGGVQVYGDVVMNHKGGADATENVLAY 120  
QY 121 EVNPNRNOEISGDYTIKAWTKPFDFFGRGNTYSDFKWRWYHFDGVDWDQSRQFQNRYYKF 180  
Db 121 EVNPNRNOEISGDYTIKAWTKPFDFFGRGNTYSDFKWRWYHFDGVDWDQSRQFQNRYYKF 180  
QY 181 RGDGKAWDEVDSENGNYDLYADYVDMDHPEVYNELRRGWGYTNTLNDGFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNYDLYADYVDMDHPEVYNELRRGWGYTNTLNDGFRIDAVKH 240  
QY 241 IKYSFTRDMLTHVRNATGKEMFAVAFKNDLGALENYLNKTNWHSVFDVPLHYNLNA 300  
Db 241 IKYSFTRDMLTHVRNATGKEMFAVAFKNDLGALENYLNKTNWHSVFDVPLHYNLNA 300  
QY 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSDQGESLESFQWFKPLAYALLITRE 360  
Db 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSDQGESLESFQWFKPLAYALLITRE 360  
QY 361 QGYPSVFGDYGYGIPTHSVPAKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPSVFGDYGYGIPTHSVPAKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
QY 421 HNSGLATIMSDGPGGKMYVGQKAGQVWHDTGNKPGTGTINADGWANFVNGGSVS 480  
Db 421 HNSGLATIMSDGPGGKMYVGQKAGQVWHDTGNKPGTGTINADGWANFVNGGSVS 480  
QY 481 IWVKR 485  
Db 481 IWVKR 485  
RESULT 12  
AAB76587  
ID ABB76587 standard; protein; 485 AA.  
XX ABB76587;  
XX 19-AUG-2002 (first entry)  
XX Termamyl-like-alpha-amylase #2.  
XX Termamyl; alpha amylase; starch liquefaction; ethanol production;  
KW textile desizing; detergent; enzyme.  
XX Bacillus sp.  
XX WO200210355-A2.  
XX 07-FEB-2002.  
XX 12-JUL-2001; 2001WO-DK000488.  
XX 01-AUG-2000; 2000DK-00001160.  
XX 12-SEP-2000; 2000DK-00001354.  
XX 10-NOV-2000; 2000DK-00001687.  
XX 26-APR-2001; 2001DK-00000655.  
XX (NOVO ) NOVOZYMES AS.  
XX Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;  
XX WPI; 2002-280633/32.  
XX N-PSDB; ABL96208.  
XX Variant of parent Termamyl-like alpha amylase, useful in detergent  
PT compositions, for starch liquefaction, ethanol production, washing and/or  
PT dish washing, and textile desizing.  
XX Claim 8; Fig 1; 90pp; English.  
XX This invention relates to variants of a parent Termamyl-like alpha-



CC amylases. These are used for starch liquefaction, ethanol production,  
 CC detergent, and textile desizing. The amylases have altered stability,  
 CC particularly at high temperatures from 70-120plusC and low pH in the  
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-  
 CC amylase  
 XX  
 SQ Sequence 485 AA;  
 Query Match 100.0%; Score 2720; DB 5; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 HHNGTGTMMQYFEWHLFNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSDVGYGA 60  
 Db 1 HHNGTGTMMQYFEWHLFNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSDVGYGA 60  
 Qy 61 YDLGLCEFNQKGTVRTKYGTRSQLESIAHALKNGVQVYGVVMMHKGADATENVLAV 120  
 Db 61 YDLGLCEFNQKGTVRTKYGTRSQLESIAHALKNGVQVYGVVMMHKGADATENVLAV 120  
 Qy 121 EVNPNRNRQELSGDYTTIEATWTKFDPGKRGNTYSDFKRWYHFDGVDQSRQFNRIYKF 180  
 Db 121 EVNPNRNRQELSGDYTTIEATWTKFDPGKRGNTYSDFKRWYHFDGVDQSRQFNRIYKF 180  
 Qy 181 RGDGKAMDWEVDSSENGYDYLMDYADVMDHDPVNNELRRGGEWYTTNTLNLDFRIDAVKH 240  
 Db 181 RGDGKAMDWEVDSSENGYDYLMDYADVMDHDPVNNELRRGGEWYTTNTLNLDFRIDAVKH 240  
 Qy 241 IKYSFTDRDLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300  
 Db 241 IKYSFTDRDLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300  
 Qy 301 SNSGNYDMAKLLNGTVVQKHPMAVTVDVNDHSDQGESLESFVQEWFKPLAYALILTRE 360  
 Db 301 SNSGNYDMAKLLNGTVVQKHPMAVTVDVNDHSDQGESLESFVQEWFKPLAYALILTRE 360  
 Qy 361 QGYPSVFYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
 Db 361 QGYPSVFYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
 Qy 421 HPNSGLATIMSDGPGGKEMVYGVQNKAGQVWHIDITGNKPGVTITNADGWANFSVNGGSVS 480  
 Db 421 HPNSGLATIMSDGPGGKEMVYGVQNKAGQVWHIDITGNKPGVTITNADGWANFSVNGGSVS 480  
 Qy 481 IWKVR 485  
 Db 481 IWKVR 485

RESULT 13  
 ABB99481  
 ID ABB99481 standard; protein; 485 AA.  
 XX  
 AC ABB99481;

DT 12-FEB-2003 (first entry)

DE Amino acid sequence of an alpha-amylase.

XX Alpha-amylase; enzyme; detergent; boric acid.

XX Alkaliphilic bacillus.

XX WO200268575-A1.

XX 06-SEP-2002.

XX 25-FEB-2002; 2002WO-US005512.

XX 28-FEB-2001; 2001US-00795211.

XX (PROC ) PROCTER & GAMBLE CO.

XX

PI Kasturi C, Wandrat MB, Song BX;  
 XX WPI; 2003-058303/05.  
 XX Aqueous liquid or gel type detergent, useful as automatic dishwashing  
 PT composition, comprises boric acid or born compound, polyhydroxy compound,  
 FT calcium ions and alpha-amylase enzyme,.  
 XX  
 XX Claim 1; Page 26-29; 36pp; English.  
 XX The present sequence represents an alpha-amylase. The enzyme is used in  
 CC detergents of the invention. The specification describes an aqueous  
 CC liquid or gel type detergent composition, which comprises boric acid or a  
 CC boron compound capable of forming boric acid in the composition, a  
 CC polyhydroxy compound, calcium ions and selected alpha-amylase enzyme. The  
 CC detergent composition is useful for stabilizing an amylase enzyme in an  
 CC aqueous liquid or gel type detergent composition. It is useful for  
 CC cleaning tableware (e.g. glassware, china, silverware, plastics),  
 CC kitchenware, household surface such as floors, bathroom fixtures and  
 CC countertops, and fabrics. It is useful as a fully formulated cleaning  
 CC powder or as an additive or speciality product that is used alone or with  
 CC other cleaning products. It is particularly useful in automatic  
 CC dishwashing machine  
 XX

SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 6; Length 485;

Best Local Similarity 100.0%; Pred. No. 3.2e-212;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLFNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSDVGYGA 60  
 Db 1 HHNGTGTMMQYFEWHLFNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSDVGYGA 60  
 Qy 61 YDLGLCEFNQKGTVRTKYGTRSQLESIAHALKNGVQVYGVVMMHKGADATENVLAV 120  
 Db 61 YDLGLCEFNQKGTVRTKYGTRSQLESIAHALKNGVQVYGVVMMHKGADATENVLAV 120  
 Qy 121 EVNPNRNRQELSGDYTTIEATWTKFDPGKRGNTYSDFKRWYHFDGVDQSRQFNRIYKF 180  
 Db 121 EVNPNRNRQELSGDYTTIEATWTKFDPGKRGNTYSDFKRWYHFDGVDQSRQFNRIYKF 180  
 Qy 181 RGDGKAMDWEVDSSENGYDYLMDYADVMDHDPVNNELRRGGEWYTTNTLNLDFRIDAVKH 240  
 Db 181 RGDGKAMDWEVDSSENGYDYLMDYADVMDHDPVNNELRRGGEWYTTNTLNLDFRIDAVKH 240  
 Qy 241 IKYSFTDRDLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300  
 Db 241 IKYSFTDRDLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300  
 Qy 301 SNSGNYDMAKLLNGTVVQKHPMAVTVDVNDHSDQGESLESFVQEWFKPLAYALILTRE 360  
 Db 301 SNSGNYDMAKLLNGTVVQKHPMAVTVDVNDHSDQGESLESFVQEWFKPLAYALILTRE 360  
 Qy 361 QGYPSVFYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
 Db 361 QGYPSVFYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
 Qy 421 HPNSGLATIMSDGPGGKEMVYGVQNKAGQVWHIDITGNKPGVTITNADGWANFSVNGGSVS 480  
 Db 421 HPNSGLATIMSDGPGGKEMVYGVQNKAGQVWHIDITGNKPGVTITNADGWANFSVNGGSVS 480  
 Qy 481 IWKVR 485  
 Db 481 IWKVR 485

RESULT 14  
 AAB30701  
 ID AAB30701 standard; protein; 834 AA.  
 XX  
 AC AAB30701;

XX

DT 02-APR-2001 (first entry)  
 XX A Bacillus pectate lyase and JP170 alpha-amylase fusion protein.  
 XX  
 XX Pectate lyase; pectinase; alpha-1,4-glycosidic linkage; pectic acid;  
 XX polygalacturonic acid; alpha-amylase.  
 XX  
 XX Synthetic.  
 OS Bacillus licheniformis.  
 OS Escherichia coli.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..29  
 FT /note= "signal peptide"  
 FT Protein 30..343  
 FT /note= "pectate lyase"  
 FT Peptide 346..349  
 FT /note= "IEGR linker"  
 FT Protein 350..834  
 FT /note= "alpha-amylase"  
 XX  
 XX WO200075344-A1.  
 XX  
 XX 14-DEC-2000.  
 XX  
 XX 31-MAY-2000; 2000WO-DK000296.  
 XX  
 XX 02-JUN-1999; 99DK-00000780.  
 PR 11-JUN-1999; 99US-0138692P.  
 XX  
 XX (NOVO ) NOVO NORDISK AS.  
 XX  
 XX Rasmussen MD, Bjoernvad ME, Diers I;  
 PI WPI; 2001-071079/08.  
 DR N-PSDB; AAC86598.  
 XX  
 XX Bacillus cells having a DNA sequence coding for a pectate lyase, a  
 PT proteolytic cleavage target site, or a polypeptide of exogenous origin  
 PT fused sequentially into one open reading frame, for producing fusion  
 PT proteins in higher yields.  
 XX  
 XX Claim 18; Page 69-73; 94pp; English.  
 XX  
 XX The present sequence represents a fusion protein of a Bacillus pectate  
 CC lyase polypeptide and a JP170 alpha-amylase polypeptide. Pectate lyase is  
 CC a pectinase which catalyses the random cleavage of alpha-1,4-glycosidic  
 CC linkages in pectic acid (polygalacturonic acid). The fusion polypeptide  
 CC is expressed using the cells of the invention. The specification  
 CC describes a cell for improved production of a fusion protein comprising a  
 CC native pectate lyase fused to an exogenous polypeptide. The cell is  
 CC preferably a gram positive cell. The cell is useful for the production of  
 CC higher yields of fusion proteins or polypeptides, which have been  
 CC difficult to obtain, such as active human antibodies  
 XX  
 XX Sequence 834 AA;  
 SQ  
 Query Match 100.0%; Score 2720; DB 4; Length 834;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-212;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HNGTGTGTMQYFEWHLPNDSNHLRDDASNLNRGITAIPPAWKGTSDNDVGYGA 60  
 DB 350 HNGTGTGTMQYFEWHLPNDSNHLRDDASNLNRGITAIPPAWKGTSDNDVGYGA 409  
 QY 61 YDLYDLGEFNQKGTVRTKGTQRLQSAIHALKNGVQVGVDMHKGADATENVLAV 120  
 DB 410 YDLYDLGEFNQKGTVRTKGTQRLQSAIHALKNGVQVGVDMHKGADATENVLAV 469  
 QY 121 EVNPNRNRNQBISGDYITIAWTKDFPGRGNVYDFKRWYHFDGVDWDQSRQFNRIYKF 180  
 DB 470 EVNPNRNRNQBISGDYITIAWTKDFPGRGNVYDFKRWYHFDGVDWDQSRQFNRIYKF 529

QY 181 RGDGKAWDEVDSENGNNDYLMYADVDMDHPEVNNELRRGWGYTNTLNDGFRIDAVKH 240  
 DB 530 RGDGKAWDEVDSENGNNDYLMYADVDMDHPEVNNELRRGWGYTNTLNDGFRIDAVKH 589  
 QY 241 IKYSFTEDMLTHVRNATGKEMFAEFKNDLGALENYLNKTNMHSVFDVPLHYNLYNA 300  
 DB 590 IKYSFTEDMLTHVRNATGKEMFAEFKNDLGALENYLNKTNMHSVFDVPLHYNLYNA 649  
 QY 301 SNSGGNYDMAKLNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKFLAYALLITRE 360  
 DB 650 SNSGGNYDMAKLNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKFLAYALLITRE 709  
 QY 361 QGYPSVFYGYGIPHTSPVAMKAKIDPILARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
 DB 710 QGYPSVFYGYGIPHTSPVAMKAKIDPILARQNFAYGTQHDYFDHNNIIGWTREGNTT 769  
 QY 421 HPNSGLATIMSDGPGGKEMVYQNKAGOVHDDITGNKPGTVTINADGWANFVNGGSVS 480  
 DB 770 HPNSGLATIMSDGPGGKEMVYQNKAGOVHDDITGNKPGTVTINADGWANFVNGGSVS 829  
 QY 481 IWVKR 485  
 DB 830 IWVKR 834  
 RESULT 15  
 AAY07392  
 ID AAY07392 standard; protein; 485 AA.  
 XX AAY07392;  
 DT 16-JUL-1999 (first entry)  
 XX  
 DE Wild type Termamyl (RTM)-like alpha-amylase protein #8.  
 XX  
 XX Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;  
 KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;  
 KW ethanol.  
 XX  
 OS Bacillus sp.  
 XX  
 XX WO9919467-A1.  
 XX  
 XX 22-APR-1999.  
 XX  
 XX 13-OCT-1998; 98WO-DK000444.  
 XX  
 XX 13-OCT-1997; 97DK-00001172.  
 XX  
 XX (NOVO ) NOVO-NORDISK AS.  
 XX  
 XX Svendsen A, Borchert TV, Bisgard-Frantzen H;  
 XX WPI; 1999-277632/23.  
 XX  
 XX Variant alpha-amylases - useful as detergents or for textile desizing or  
 PT starch liquefaction.  
 XX  
 XX Disclosure; Page 74-76; 93pp; English.  
 XX  
 XX This sequence represents the parent sequence for new variants of a parent  
 CC Termamyl-like alpha-amylase with alpha-amylase activity. The variants  
 CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase  
 CC from either of two Bacillus species in WO9526397, B. stearothermophilus,  
 CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-  
 CC amylase variants are detergent additives for use in detergents for  
 CC dishwashing, manual or automatic laundry. The variants can also be used  
 CC for textile desizing or starch liquefaction (e.g. for production of  
 CC sweeteners or ethanol)  
 XX  
 XX Sequence 485 AA;  
 SQ  
 Query Match 99.7%; Score 2712; DB 2; Length 485;

Best Local Similarity 99.8%; Pred. No. 1.4e-211;		Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	HHNGTNGTMMQYFEWHLFNDGNHWNRLRDDASNLNRNGITAIWI	PPAWKGTSONDVG YGA 60
Db	1	HHNGTNGTMMQYFEWHLFNDGNHWNRLRDDASNLNRNGITAIWI	PPAWKGTSONDVG YGA 60
Qy	61	YDLYDLGEFNQKGTVRTKYGTRSQLESIAIHALKXNGVQVYGDV	VVNNHKGADATENVLAV 120
Db	61	YDLYDLGEFNQKGTVRTKYGTRSQLESIAIHALKXNGVQVYGDV	VVNNHKGADATENVLAV 120
Qy	121	EVAPNNENQETSGDYTTIEATWKDFPGRGNTYSDFKRWVHF	DGVDQSRQFONRIYKF 180
Db	121	EVAPNNENQETSGDYTTIEATWKDFPGRGNTYSDFKRWVHF	DGVDQSRQFONRIYKF 180
Qy	181	RGDGKAWDWEVDSSENGNYDILMYADVDMDHPEVVNELRR	GEWYTTNLDGFRIDAVKH 240
Db	181	RGDGKAWDWEVDSSENGNYDILMYADVDMDHPEVVNELRR	GEWYTTNLDGFRIDAVKH 240
Qy	241	IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNK	TNNHVSFVDFPLHYNLYNA 300
Db	241	IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNK	TNNHVSFVDFPLHYNLYNA 300
Qy	301	SNSCGNYDMAKLNLNGTVVQKHPMHAVTFVDNHDSPGES	LESFVOEWFKPLAYALILTRE 360
Db	301	SNSCGNYDMAKLNLNGTVVQKHPMHAVTFVDNHDSPGES	LESFVOEWFKPLAYALILTRE 360
Qy	361	QGYPSVFGDYGYGIPTHSVPAKAKIDPILAEARONFAYG	TQHDYFDHNNIIGWTREGNTT 420
Db	361	QGYPSVFGDYGYGIPTHSVPAKAKIDPILAEARONFAYG	TQHDYFDHNNIIGWTREGNTT 420
Qy	421	HPNSGLATIMSDGPGGKMWYVGQNKAGQVWHDDITGNK	PGTVTITINADGWANFSVNGGSVS 480
Db	421	HPNSGLATIMSDGPGGKMWYVGQNKAGQVWHDDITGNK	PGTVTITINADGWANFSVNGGSVS 480
Qy	481	IWKVR 485	
Db	481	IWKVR 485	

Search completed: October 7, 2004, 00:12:13  
Job time : 60.5516 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds  
(without alignments)  
3290.816 Million cell updates/sec

Title: US-09-925-576C-4  
Perfect score: 2720  
Sequence: 1 HHNGTNGTMQYFEWHLPND.....ADGWANFSVNGSGSVSIWKR 485

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2440	89.7	516	2	082839
2	1984	72.9	533	2	09AQ54
3	1976	72.6	513	16	081A54
4	1967	72.3	513	16	081VJ4
5	1910.5	70.2	613	2	059222
6	1903	70.0	519	2	03RQ78
7	1899.5	69.5	549	2	031193
8	1894.5	69.3	521	2	071034
9	1884.5	69.3	549	2	09KW76
10	1860.5	68.4	501	2	093148
11	1556.5	57.2	507	16	087HG6
12	1374	50.5	481	16	089IF1
13	1373	50.5	493	2	030657
14	1296.5	47.7	486	16	08DT08
15	1279.5	47.0	488	16	08EOM2
16	1276.5	46.9	488	16	08E696

17	1267	46.6	484	16	Q97Q49	Q97Q49 streptococc
18	1265	46.5	484	16	Q8DPC8	Q8DPC8 streptococc
19	1257.5	46.2	485	2	O68875	O68875 streptococc
20	1245	45.8	492	16	Q8YU21	Q8YU21 anabaena sp
21	1238.5	45.5	485	2	Q53786	Q53786 streptococc
22	1235.5	45.4	484	2	O50583	O50583 streptococc
23	1143	42.0	491	16	Q9CG59	Q9CG59 lactococcu
24	1104	40.6	506	16	Q8U916	Q8U916 agrobacteri
25	1072	39.4	494	16	Q8Z5S5	Q8Z5S5 salmonella
26	1071	39.4	495	16	Q8XBB6	Q8XBB6 escherichia
27	1069	39.3	495	16	Q8FGL8	Q8FGL8 escherichia
28	1062	39.0	495	16	Q7UAB0	Q7UAB0 shigella fl
29	1060	39.0	495	16	Q83R40	Q83R40 shigella fl
30	1027.5	37.8	529	3	Q877B1	Q877B1 aspergillus
31	507.5	18.7	461	1	O33476	O33476 pyrococcus
32	506	18.6	461	1	Q8NKR4	Q8NKR4 thermococcu
33	492	18.1	460	1	Q9P9L0	Q9P9L0 pyrococcus
34	492	18.1	460	1	O08452	O08452 pyrococcus
35	492	18.1	473	17	Q8U319	Q8U319 pyrococcus
36	490	18.0	461	1	Q8NKR5	Q8NKR5 thermococcu
37	485	17.8	469	1	O50200	O50200 thermococcu
38	480	17.6	432	14	Q8JZK3	Q8JZK3 uncultured
39	467	17.2	457	1	Q93647	Q93647 thermococcu
40	322.5	11.9	482	2	Q60051	Q60051 thermoactin
41	298.5	11.0	421	10	Q7X9T1	Q7X9T1 phaseolus a
42	296	10.9	420	10	Q9ZP43	Q9ZP43 phaseolus v
43	293	10.8	424	10	Q8LP27	Q8LP27 pharbitis n
44	288	10.6	423	10	Q42678	Q42678 cuscata ref
45	285	10.5	416	10	Q8LJQ6	Q8LJQ6 musa acumin

## ALIGNMENTS

### RESULT 1

ID	082839	PRELIMINARY;	PRT;	516 AA.
AC	082839;			
DT	01-NOV-1998 (Tremblrel. 08, Created)			
DT	01-NOV-1998 (Tremblrel. 08, Last sequence update)			
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)			
DE	Amylase.			
OS	Bacillus sp.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1409;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=KSM-1378;			
RX	MEDLINE=98342096; PubMed=9675143;			
RA	Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,			
RA	Ozaki K., Ito S.;			
RT	"Improved thermostability of a Bacillus alpha-amylase by deletion of			
RL	an arginine-glycine residue is caused by enhanced calcium binding."			
RL	Biochem. Biophys. Res. Commun. 248:372-377 (1998).			
DR	EMBL; AB008763; BAA32431.1; -			
DR	HSSP; P06278; 1VJS.			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha amyl cat.			
DR	InterPro; IPR006589; Alp_ami1 cat sub.			
DR	InterPro; IPR006046; Glyco hydro_13.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAMYLASE.			
DR	SMART; SMO0642; Amy; 1.			
SQ	SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;			

Query Match	89.7%;	Score 2440;	DB 2;	Length 516;
Best Local Similarity	86.6%;	Pred.No. 6.3e-148;		
Matches 420;	Conservative 40;	Mismatches 25;	Indels 0;	Gaps 0;
Qy	1	HHNGTNGTMQYFEWHLPNDGNHWNRLRDDASNLNRNGITAIWIPPAWKGTSDNDVGYGA	60	
Db	32	HHNGTNGTMQYFEWHLPNDGNHWNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGYGA	91	

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QY 61 YDYLDELGEFNQKGTVRTKYKTRTSQLESIAIHALKNNNGVQVYGDVVMNHHKGGADATENVLAV 120
DB 92 YDYLDELGEFNQKGTVRTKYKTRSQLOQAVTSLKNNNGLOVYGDVVMNHHKGGADGTWNAV 151
QY 121 EVNPNRNQISGDIYTTIETAWTKDFPGRGNTYSDFKRWYTHFDGVWDQSRQFQNRYYKFP 180
DB 152 EVNRSNRNQBISGEYTTIETAWTKDFPGRGNTSHSNFKRWYTHFDGTDWDQSRQLQNKIYKF 211
QY 181 RGPCKAWDEVDSENGNYDYLMAVDMDHPEVNVNLRWGEWYTNLNDGFRIDAVKH 240
DB 212 RGTGKAWDEVDSENGNYDYLMAVDMDHPEVNVNLRWGEWYTNLNDGFRIDAVKH 271
QY 241 IKYSFTFDMTLTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHNSVDFVPLHYNLNLA 300
DB 272 IKYSFTFDMTLTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHNSVDFVPLHYNLNLA 331
QY 301 SNSSGNYDMAKLNGTVVQKHPHMAVTFVDNHDSPQGESLESFVQEMFKPLAYALILTRE 360
DB 332 SNSSGYPDMRNILNGSVVQKHPHMAVTFVDNHDSPQGESLESFVQSWFKPLAYALILTRE 391
QY 361 QGYPSVFGYDYGIPHTSVDPAMKAKIDPILBARONFAYGTHQHDYFDHNNIIGTWREGNTT 420
DB 392 QGYPSVFGYDYGIPHTSGVPSMKSKDPLQARQTYAYGTHQHDYFDHNNIIGTWREGDSS 451
QY 421 HPNSGLATIMSDGPGGKMMYVGNKAGOVVHDIITGNKPGCTVTINADGWANFVNGSGSVS 480
DB 452 HPNSGLATIMSDGPGGKMMYVGNKAGOVVHDIITGNRSGTGTVTINADGWANFVNGSGSVS 511
QY 481 IWVKR 485
DB 512 VVVKQ 516
```

RESULT 2

Q9AQ54

ID Q9AQ54 PRELIMINARY; PRT; 533 AA.

AC Q9AQ54;

DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Alpha-amylase.

OS Bacillus megaterium.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1404;

RN [1]

RP SEQUENCE FROM N.A.

RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W., Park K.-H.,

RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium KSM B-404."

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF220440; AAK00598.1; -.

DR HSSP; P06278; 1VJS.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha\_amyl\_cat.

DR InterPro; IPR006589; Alp\_amyl\_cat\_sub.

DR Pfam; PF00128; alpha-amylase; 1.

DR SMART; SM00642; Aamy; 1.

SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 72.9%; Score 1984; DB 2; Length 533;  
Best Local Similarity 71.2%; Pred. No. 9.1e-119;  
Matches 344; Conservative 58; Mismatches 77; Indels 4; Gaps 2;

```
QY 6 NGTMMQYFEWHLNDGNHNRDRDASNLNRNGITAIWIPPAWKGTSONDVGAYDLYD 65
DB 52 NGTMMQYFEWYANDGNHNRDLTDAENLAQKITSWIPPAKGTQNDVGAYDLYD 111
QY 66 LGSEFNQKGTVRTKYKTRTSQLESIAIHALKNNNGVQVYGDVVMNHHKGGADATENVLAVNPN 125
DB 112 LGSEFNQKGTVRTKYKTKAQLKSAIDALHKKNIIDVYGDVVMNHHKGGADYTETVTAVEVDPS 171
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QY 126 NRNOEISGDYTTIETAWTKDFPGRGNTYSDFKRWYTHFDGVWDQSRQFQNRYYKFRGDGK 185
DB 172 NRNVESGDYETISAWTGFNPGGDSYSNFKWKYTHFDGTDWDEGRKL-NRIYKFRGIGK 230
QY 186 AMDWEVDSNGNYDYLMAVDMDHPEVNVNLRWGEWYTNLNDGFRIDAVKHIKYSP 245
DB 231 AMDWEVSSNGNYDYLMAVDLDFHDPDVANEMKMGCTWTYANELNLDGFRIDAVKHIDHEY 290
QY 246 TRDMLTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHNSVDFVPLHYNLNNA NSGG 305
DB 291 LRDMNVHVRQQTKEMFAVAEYQNDIQTLNNYLAKNNVNSQSFDAPLHYNFHYASRGNG 350
QY 306 NYDMAKLNGTVVQKHPHMAVTFVDNHDSPQGESLESFVQEMFKPLAYALILTREOCYPS 365
DB 351 NYDMRNILAGTVVANHPTLAVTLVENHDSQPQGESLESVSPWFKPLAYAFILTRAEGYPS 410
QY 366 VFYGDYIGYPTHS---VPAMKAKIDPILBARONFAYGTHQHDYFDHNNIIGTWREGNTTTHP 422
DB 411 VFYGDYIGTKGNSYEIPALKDKIDPILTKARKNYAYGTQDYFDHDPDVIQWTRGDSVHA 470
QY 423 NSGLATIMSDGPGGKMMYVGNKAGOVVHDIITGNKPGCTVTINADGWANFVNGSGSVSIW 482
DB 471 NSGLATLISDGGGAKWMDVGNKNAGEIWIYDITGNQTNQTNVINKDGMGQFQVSGGVSIIY 530
QY 483 VKR 485
DB 531 VQR 533
```

RESULT 3

Q81AS4

ID Q81AS4 PRELIMINARY; PRT; 513 AA.

AC Q81AS4;

DT 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).

GN BC3482.

OS Bacillus cereus (strain ATCC 14579 / DSM 31).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=226900;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22608415; PubMed=12721630;

RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapratral V., Bhattacharyya A., Resnik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goitsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.

RT "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis."

RL Nature 423:87-91(2003).

DR EMBL; AB017009; AAP10417.1; -.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha\_amyl\_cat.

DR InterPro; IPR006589; Alp\_amyl\_cat\_sub.

DR Pfam; PF00128; alpha-amylase; 1.

DR SMART; SM00642; Aamy; 1.

KW Glycosidase; Hydrolase; Complete proteome.

SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BFF9FF6 CRC64;

Query Match 72.6%; Score 1976; DB 16; Length 513;  
Best Local Similarity 71.0%; Pred. No. 2.8e-118;  
Matches 343; Conservative 57; Mismatches 79; Indels 4; Gaps 2;

```
QY 6 NGTMMQYFEWHLNDGNHNRDRDASNLNRNGITAIWIPPAWKGTSONDVGAYDLYD 65
DB 32 NGTMMQYFEWYANDGNHNRDLTDAENLAQKITSWIPPAKGTQNDVGAYDLYD 91
QY 66 LGSEFNQKGTVRTKYKTRTSQLESIAIHALKNNNGVQVYGDVVMNHHKGGADATENVLAVNPN 125
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Db 92 LGFENQKGTVRTKTYGTGAQKLSAIDALHKKNDIVYGVVNMHKGADYTETVTVAEVDPS 151
Qy 126 NRQOEISGDTTIEAWTKDFPGRGNTYSDFKRWYHFDGVDWDSQSFQNRIRYKFRGDGK 185
Db 152 NRNVESGDYEISAWTGFNPGRGDSYSNFKWKYHFDGTDWDSGRKL-NRIYKFRGIGK 210
Qy 186 AWDWEVDSNGNDYLMYADVMDHPEVNNELRWGEWYTNLNLDFGRIDAVKHIXYSP 245
Db 211 AWDWEVDSNGNDYLMYADLDFDHPDVANEMKKGWYANLNLDFGRIDAVKHIDHEY 270
Qy 246 TRDLWTHVRNATGKEMFAVAFWKNLIDGALENYLNKTNMHSVDFVPLHYNLYNASGG 305
Db 271 LRDNWVNRQGTGKEMFTVAEYQNDIOTLNNYLAKVYNQSVDFDPLHYNFHYASTGNG 330
Qy 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQWFKPLAYALILITREQGYPS 365
Db 331 NYDMRNILKGTVANHTPLAVTLVENHDSQPGSLESVSWPFPKPLAYAFILITRAEGYPS 390
Qy 366 VFYGDYIGTGSNYSYEIPALKDKIDPILTKARKPAYGTQRDYFDPDVGWTRREGDSVHA 422
Db 391 VFYGDYIGTGSNYSYEIPALKDKIDPILTKARKPAYGTQRDYFDPDVGWTRREGDSVHA 450
Qy 423 NSGLATIMSDPGGKWMYVQKNGKAGOVHMDITGNKFTVTINADGANFVSGSVSIW 482
Db 451 NSGLATILISDGGKWMVQKNGNAGBVMYDITGNQNTVTINKDGRGQFVSGSVSIY 510
Qy 483 VKR 485
Db 511 VQ 513

RESULT 4
Q81YJ4 PRELIMINARY; PRT; 513 AA.
ID Q81YJ4
AC Q81YJ4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzaple E.K., Ostad O.A., Helgason E., Rikstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Winn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomsen B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Complete proteome.
KW SEQUENCE 513 AA; 58445 MW; 5586DEFF28FD159B CRC64;
SQ

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Query Match

72.3%; Score 1967; DB 16; Length 513;

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Best Local Similarity 70.6%; Pred. No. 1.1e-117;
Matches 341; Conservative 57; Mismatches 81; Indels 4; Gaps 2;

Qy 6 NGTMQYFEWHLNDGNNHNRRLRDDASNLNRGRTITAIWIPPAWKGTSQNDVGYGAYDLYD 65
Db 32 NGTLMQYFEWYAPSDRNNHNRRLRTDAENLAQKGSITWIPPAWKGTTQNDVGYGAYDLYD 91
Qy 66 LGFENQKGTVRTKTYGTGRSLESALHAKNNGVQYGVVNMHKGADATENLVAVENPN 125
Db 92 LGFENQKGTVRTKTYGTGAQKLSAIEALHKNQIDVYGVVNMHKGADYTETVTVAEVDN 151
Qy 126 NRQOEISGDTTIEAWTKDFPGRGNTYSDFKRWYHFDGVDWDSQSFQNRIRYKFRGDGK 185
Db 152 NRNVESGDYEISAWTGFNPGRGDSYSNFKWKYHFDGTDWDSGRKL-NRIYKFRGIGK 210
Qy 186 AWDWEVDSNGNDYLMYADVMDHPEVNNELRWGEWYTNLNLDFGRIDAVKHIXYSP 245
Db 211 AWDWEVDSNGNDYLMYADLDFDHPDVANEMKKGWYANLNLDFGRIDAVKHIDHEY 270
Qy 246 TRDLWTHVRNATGKEMFAVAFWKNLIDGALENYLNKTNMHSVDFVPLHYNLYNASGG 305
Db 271 LRDNWVNRQGTGKEMFTVAEYQNDIOTLNNYLAKVYNQSVDFDPLHYNFHYASTGNG 330
Qy 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQWFKPLAYALILITREQGYPS 365
Db 331 NYDMRNILKGTVANHTPLAVTLVENHDSQPGSLESVSWPFPKPLAYAFILITRAEGYPS 390
Qy 366 VFYGDYIGTGSNYSYEIPALKDKIDPILTKARKPAYGTQRDYFDPDVGWTRREGDTHP 422
Db 391 VFYGDYIGTGSNYSYEIPALKDKIDPILTKARKPAYGTQRDYFDPDVGWTRREGDTHP 450
Qy 423 NSGLATIMSDPGGKWMYVQKNGKAGOVHMDITGNKFTVTINADGANFVSGSVSIW 482
Db 451 NSGLATILISDGGKWMVQKNGNAGBVMYDITGNQNTVTINKDGRGQFVSGSVSIY 510
Qy 483 VKR 485
Db 511 VQ 513

RESULT 5
Q59222 PRELIMINARY; PRT; 613 AA.
ID Q59222
AC Q59222;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.2.1).
GN AMY.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin L.-L., Chu W.S., Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22045; AAA63900.1; -.
DR HSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0008477; P:purine nucleosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat_sub.
DR InterPro; IPR006046; Glyco hydro 13.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF00686; CBM 20; 1.
DR PRINTS; PRO0110; ALPHAMYLASE.
DR ProDom; PD001568; CBD 4; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.

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SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;
Query Match 70.2%; Score 1910.5; DB 2; Length 613;
Best Local Similarity 69.2%; Pred. No. 5.4e-114;
Matches 332; Conservative 63; Mismatches 84; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLFNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLYD 65
DB 36 NETMMQYFEWDLNDGTLTKVKNRANLSSGITALMLPPAYKGTSONDVGYGVYDLYD 95
QY 66 LGFEFNQKGTVRTKYGTRSQLESAIHALKNNGVQYGVVMMHKGADATENVLAVERNPN 125
DB 96 LGFEFNQKGTVRTKYGTRSQLESAIHALKNNGVQYGVVMMHKGADATENVLAVERNPN 125
QY 126 NRNQEISGDYTIKAWTKFDPGRGNTYSDFKRWVYHFDGVDWDSRQFQNRILYKFRGDGK 185
DB 156 NRNQESGTGQIQAQWTKFDPGRGNTYSDFKRWVYHFDGVDWDSRQFQNRILYKFRSTGK 214
QY 186 AWDWEVDSNGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLDDGFRIDAVKHIKYSF 245
DB 215 AWDWEVDSNGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLDDGFRIDAVKHIKYSF 245
QY 246 TRDMLTHVRNATGKEMPAFAVAFKWNKDLGALENYLNKTNHNSVFDVPLHYNLNANSNG 305
DB 275 TRDMLTHVRNATGKEMPAFAVAFKWNKDLGALENYLNKTNHNSVFDVPLHYNLNANSNG 305
QY 306 NYDMAKLINGTVVQKHPMHAVTFVDNHDSPGESLESFVQWFKPLAYALILTREGQYPS 365
DB 335 YFDMRYLLNLTMLKQDPSLAVTLVDNHDTPQGSQSWVEPWFKPLAYAFILTRQEGYPC 394
QY 366 VFGYDYGIPKYNIPGLKSKDILLARRDYAGTQRDIDHODIIGTWREGIDTKPNSG 454
DB 395 VFGYDYGIPKYNIPGLKSKDILLARRDYAGTQRDIDHODIIGTWREGIDTKPNSG 454
QY 426 LATIMSDGPGGKEMMYVQGNKAGQVWHDITGNKPGTITINADGWANFNVNGGVSIVWKR 485
DB 455 LATIMSDGPGGKEMMYVQGNKAGQVWHDITGNKPGTITINADGWANFNVNGGVSIVWKR 485

RESULT 6
Q9RQT8 PRELIMINARY; PRT; 519 AA.
AC Q9RQT8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF0567.1; --
DR HSSP; P06278; 1VJ5.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT CHAIN 58 519 RAW STARCH DIGESTING AMYLASE.
SQ SEQUENCE 519 AA; 58337 MW; 3E688A4DF98B163 CRC64;

Query Match 70.0%; Score 1903; DB 2; Length 519;
Best Local Similarity 67.8%; Pred. No. 1.3e-113;
Matches 328; Conservative 72; Mismatches 80; Indels 4; Gaps 2;

SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;
Query Match 70.2%; Score 1910.5; DB 2; Length 613;
Best Local Similarity 69.2%; Pred. No. 5.4e-114;
Matches 332; Conservative 63; Mismatches 84; Indels 1; Gaps 1;

QY 5 TNGTMMQYFEWHLFNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLY 64
DB 37 TNGTMMQYFEWHLFNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLY 96
QY 65 DLGEFNQKGTVRTKYGTRSQLESAIHALKNNGVQYGVVMMHKGADATENVLAVERNPN 124
DB 97 DLGEFNQKGTVRTKYGTRSQLESAIHALKNNGVQYGVVMMHKGADATENVLAVERNPN 156
QY 125 NRNQEISGDYTIKAWTKFDPGRGNTYSDFKRWVYHFDGVDWDSRQFQNRILYKFRGDG 184
DB 157 NRNQESGTGQIQAQWTKFDPGRGNTYSDFKRWVYHFDGVDWDSRQFQNRILYKFRSTG 215
QY 185 KAWDEVDSENGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLDDGFRIDAVKHIKYS 244
DB 216 KAWDEVDSENGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLDDGFRIDAVKHIKYS 275
QY 245 FTRDMLTHVRNATGKEMPAFAVAFKWNKDLGALENYLNKTNHNSVFDVPLHYNLNANSNG 304
DB 276 FTRDMLTHVRNATGKEMPAFAVAFKWNKDLGALENYLNKTNHNSVFDVPLHYNLNANSNG 335
QY 305 GNYDMAKLINGTVVQKHPMHAVTFVDNHDSPGESLESFVQWFKPLAYALILTREGQY 364
DB 336 GNYDMAKLINGTVVQKHPMHAVTFVDNHDSPGESLESFVQWFKPLAYALILTREGQY 395
QY 365 SVFYGDY--GIPKYNIPGLKSKDILLARRDYAGTQRDIDHODIIGTWREGIDTKPNSG 421
DB 396 SVFYGDY--GIPKYNIPGLKSKDILLARRDYAGTQRDIDHODIIGTWREGIDTKPNSG 455
QY 422 PMSGLATIMSDGPGGKEMMYVQGNKAGQVWHDITGNKPGTITINADGWANFNVNGGVS 481
DB 456 AKSGLATIMSDGPGGKEMMYVQGNKAGQVWHDITGNKPGTITINADGWANFNVNGGVS 515
QY 482 WKCR 485
DB 516 WKQQ 519

RESULT 7
O31193 PRELIMINARY; PRT; 549 AA.
AC O31193
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha amylase.
OS Ami.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF032864; AAB86961.1; --
DR PIR; A54541; A54541.
DR HSSP; P06278; 1VJ5.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

Query Match 69.5%; Score 1889.5; DB 2; Length 549;
Best Local Similarity 67.7%; Pred. No. 1e-112;
Matches 325; Conservative 73; Mismatches 81; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLFNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLYD 65
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Db 39 NGTMMQYFEWYLPDDGLTWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 98
QY 66 LGBFNQKGTVRTKYTGTRTSQLESALHALKNNGVQYVGVVNMHKGADATENLVAVEVNP 125
Db 99 LGBFNQKGTVRTKYTGTRTSQLESALHALKNNGVQYVGVVNMHKGADATENLVAVEVNP 158
QY 126 NRQNEISGDTYIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDSQROFQNRYYKFRGDGK 185
Db 159 DRQNEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
QY 186 AWDWEVDSNGNDYLMYADVDMDHPEVNVNELRWGEWYTNLTNLDGFRIDAVKHKYSF 245
Db 218 AWDWEVDTENGNDYLMYADVDMDHPEVNVTELKNWGWYNTTNDGFRDLDAVKHIFSF 277
QY 246 TRDWLTHVRNATGEMFAVAFWKNDLGCALENYLNKTNWHSVDFVPLHYNLYNASGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYNSYDINKLHNYITKTNGTMSLFDAPLHNFYTASKSGG 337
QY 306 NYDMAKLLNGTGVQKHPMHAVTFVDNHDSDQGESLESFVQWFKPLAYALILTREQGYPS 365
Db 338 AFDMRTLTMTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEGYPC 397
QY 366 VFYGDYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTHTPNSG 425
Db 398 VFYGDYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTHTPNSG 457
QY 426 LATIMSDPGGKMWYGVQKAGQVHDDITGNKPGTGTINADGWANFVSGSVIWK 485
Db 458 LAALITDGPCKMWYGVQKAGQVHDDITGNKPGTGTINADGWANFVSGSVIWK 517

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## RESULT 8

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P71034
ID P71034 PRELIMINARY; PRT; 521 AA.
AC P71034;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
RT thermostable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AB18785.1; -.
DR HSP; P06278; IYUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
DR SIGNAL.
FT SIGNAL. 1 34 POTENTIAL.
FT CHAIN 35 521 ALPHA-AMYLASE.
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;

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Query Match 69.3%; Score 1884.5; DB 2; Length 521;
Best Local Similarity 67.5%; Pred. No. 2e-112;
Matches 324; Conservative 73; Mismatches 82; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWYLPDDGLTWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGLTWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 98

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QY 66 LGBFNQKGTVRTKYTGTRTSQLESALHALKNNGVQYVGVVNMHKGADATENLVAVEVNP 125
Db 99 LGBFNQKGTVRTKYTGTRTSQLESALHALKNNGVQYVGVVNMHKGADATENLVAVEVNP 158
QY 126 NRQNEISGDTYIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDSQROFQNRYYKFRGDGK 185
Db 159 DRQNEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
QY 186 AWDWEVDSNGNDYLMYADVDMDHPEVNVNELRWGEWYTNLTNLDGFRIDAVKHKYSF 245
Db 218 AWDWEVDTENGNDYLMYADVDMDHPEVNVTELKNWGWYNTTNDGFRDLDAVKHIFSF 277
QY 246 TRDWLTHVRNATGEMFAVAFWKNDLGCALENYLNKTNWHSVDFVPLHYNLYNASGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYNSYDINKLHNYITKTNGTMSLFDAPLHNFYTASKSGG 337
QY 306 NYDMAKLLNGTGVQKHPMHAVTFVDNHDSDQGESLESFVQWFKPLAYALILTREQGYPS 365
Db 338 AFDMRTLTMTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEGYPC 397
QY 366 VFYGDYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTHTPNSG 425
Db 398 VFYGDYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTHTPNSG 457
QY 426 LATIMSDPGGKMWYGVQKAGQVHDDITGNKPGTGTINADGWANFVSGSVIWK 485
Db 458 LAALITDGPCKMWYGVQKAGQVHDDITGNKPGTGTINADGWANFVSGSVIWK 517

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## RESULT 9

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Q9KMY6
ID Q9KMY6 PRELIMINARY; PRT; 549 AA.
AC Q9KMY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase (SC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSP; P06278; IYUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
DR Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E6D6F9120BCE CRC64;

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Query Match 69.3%; Score 1884.5; DB 2; Length 549;
Best Local Similarity 67.5%; Pred. No. 2.2e-112;
Matches 324; Conservative 73; Mismatches 82; Indels 1; Gaps 1;

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QY 6 NGTMMQYFEWYLPDDGLTWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGLTWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 98
QY 66 LGBFNQKGTVRTKYTGTRTSQLESALHALKNNGVQYVGVVNMHKGADATENLVAVEVNP 125
Db 99 LGBFNQKGTVRTKYTGTRTSQLESALHALKNNGVQYVGVVNMHKGADATENLVAVEVNP 158
QY 126 NRQNEISGDTYIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDSQROFQNRYYKFRGDGK 185

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Db 159 DRNQESGTYQIQAWTKFDPPGRGNTYSSFKWRYHFDGVDWDESRKL-SRIYKFRGIGK 217
Qy 186 AWDEVDSENGNTDYLMYADVDMDHPVNNELRWGEWYTNLNLGDFRIDAVKHLYKSF 245
Db 218 AWDEVDTEGNTDYLMYADLMDHPVNTLKNWGWYNTNIDGFRDLDAVKHLYKSF 277
Qy 246 TRDWLTHVRNATGKEMFAVAFWKNDLGALENLKNMNHNSVDPVPLHYNLYNASNGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYNSYDINKLHNITKINGTMSLFDAPLHNKFTASKSGG 337
Qy 306 NYDMAKLLNGTVVQKHPMHAFTVDNHDSPGESLESFVQEWFKPLAYAILLTREQYPS 365
Db 338 AFDMRTLMTNLMKQDPTLAVTFVDNHDTPFGQALOSWDPWFKPLAYAIFILTRQEGYFG 397
Qy 366 VFYGDYGIPTHSVPAMKAKIDPLEARONFAYGTOHDYFDHNIIGWTREGNTHPNSG 425
Db 398 VFYGDYGIPTHSVPAMKAKIDPLEARONFAYGTOHDYFDHNIIGWTREGNTHPNSG 457
Qy 426 LATIMSDGPGGKWMYVGNQKAGOVVHDDITGNKPGTGTINADGWANFVNGGSGSVIWKVR 485
Db 458 LAALITDGPCKGSKWYVGNQKAGOVVHDDITGNKPGTGTINADGWANFVNGGSGSVIWKVR 517

RESULT 10
Q93I48 PRELIMINARY; PRT; 501 AA.
AC Q93I48;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYK38.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayashi Y.;
RT "Isolation of a new Bacillus alpha-amylase.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051102; BAB71820.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha-amyl cat.
DR Pfam; PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

Query Match 68.4%; Score 1860.5; DB 2; Length 501;
Best Local Similarity 66.5%; Pred. No. 6.6e-111;
Matches 321; Conservative 71; Mismatches 88; Indels 3; Gaps 2;

Qy 3 NGTGTMMQYFEWHLNDGNHNRRLDDASNLNRGITAIWIIPPAWKGT-SQNDVGYGAYD 62
Db 22 DGLNGTMMQYFEWHLNDGNHNRRLDDAALSDAGITAIWIIPPAWKGSQADVGYGAYD 81
Qy 63 LYDLGEFNQKGTVRTKYGTSQLESAIHALKNGGVQYGDVVMNHKGGADATENLAVEV 122
Db 82 LYDLGEFNQKGTVRTKYGTSQLESAIHALKNGGVQYGDVVMNHKGGADATENLAVEV 141
Qy 123 NPNNRNQEISGDYTIETAWTKFDPPGRGNTYSDPKRWYHFDGVDWDSRQFQNRKYKFRG 182
Db 142 NPTNRNQDLSGATIDAWTGDFSGRNAYSDFKRWYHFDGVDWDSRQFQNRKYKFRG 200
Qy 183 DGKADWEVDSENGNTDYLMYADVDMDHPVNNELRWGEWYTNLNLGDFRIDAVKHLYK 242
Db 201 TN--WNWRVDEENGNTDYLLIGSNIDFSHPVQDELKDWGSWFTDELDDGRLDAIKHP 258
Qy 243 YSFTRDWLTHVRNATGKEMFAVAFWKNDLGALENLKNMNHNSVDPVPLHYNLYNASN 302
Db 259 FWTSWVRHQRNEADQDLFVGEYWKVDVGALEFTEIDENWENMSLFDVPLNFTNFRASQ 318
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Qy 303 SGNVDMAKLLNGTVVQKHPMHAFTVDNHDSPGESLESFVQEWFKPLAYAILLTREQG 362
Db 319 QGSGYDMRNLRLGSLVEAHPMHAFTVDNHDTPQGESLESWADWPKPLAYATILTRREG 378
Qy 363 YPSVFYGDYGIPTHSVPAMKAKIDPLEARONFAYGTOHDYFDHNIIGWTREGNTHP 422
Db 379 YPNVFYGDYGIPTHSVPAMKAKIDPLEARONFAYGTOHDYFDHNIIGWTREGNTHP 438
Qy 423 NSGLATIMSDGPGGKWMYVGNQKAGOVVHDDITGNKPGTGTINADGWANFVNGGSGSVI 482
Db 439 NSGLATIMSDGPGGKWMYVGNQKAGOVVHDDITGNKPGTGTINADGWANFVNGGSGSVI 498
Qy 483 VKR 485
Db 499 VNQ 501

RESULT 11
Q87HG6 PRELIMINARY; PRT; 507 AA.
AC Q87HG6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN VPA0999.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62342.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha-amyl cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

Query Match 57.2%; Score 1556.5; DB 16; Length 507;
Best Local Similarity 57.1%; Pred. No. 1.8e-91;
Matches 280; Conservative 75; Mismatches 116; Indels 19; Gaps 7;

Qy 4 GTNGTMMQYFEWHLNDGNHNRRLDDASNLNRGITAIWIIPPAWKGT-SQNDVGYGAYD 62
Db 24 GQGTMMQYFEWHLNDGNHNRRLDDASNLNRGITAIWIIPPAWKGT-SQNDVGYGAYD 83
Qy 63 LYDLGEFNQKGTVRTKYGTSQLESAIHALKNGGVQYGDVVMNHKGGADATENLAVEV 122
Db 84 MYDLGEFDQKGSVRTKYGTSQLESAIHALKNGGVQYGDVVMNHKGGADATENLAVEV 143
Qy 123 NPNNRNQEISGDYTIETAWTKFDPPGRGNTYSDPKRWYHFDGVDWDSRQFQNRKYKFRG 182
Db 144 DWDNRNIEL-GDKWIEAWVEFPGRNDKYSNFHWTYHFDGVDWDSRQFQNRKYKFRG 201
Qy 183 DGKADWEVDSENGNTDYLMYADVDMDHPVNNELRWGEWYTNLNLGDFRIDAVKHLYK 242
Db 202 EGKADWEVSSKNGYDYLMDLMDHPVNNELRWGEWYTNLNLGDFRIDAVKHLYK 261
Qy 243 YSFTRDWLTHVRNATGKEMFAVAFWKNDLGALENLKNMNHNSVDPVPLHYNLYNASN 302
Db 262 YOYQLEWDHDLRWKTKELFTVGEYWNVDVNLHNFITKSGMSLFDAPLHMFNASK 321
Qy 303 SGNVDMAKLLNGTVVQKHPMHAFTVDNHDSPGESLESFVQEWFKPLAYAILLTREQG 362
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301	QNRDFDNR	TFDDSLVD	NPAYAVT	FVENHDT	QSGALES	RVDFWFK	PLAYGLI	LLRQOG	360
	..	:	:	:	:	:	:	:	:
363	YPSVFYGDY	GIP~THS	VPAMKAD	PTLEARON	PAYGTO	HDYFD	PHNIIG	WTREGNTH	421
361	TPCLFYGDY	YGIQGF	QGFQSF	KFVIDR	KMAELR	ONVVF	GKVDYF	THSCIG	WTCLGDEH
422	PNSGLAT	IMSDG	PGGEK	WMYVQ	NKAGQ	QVHDI	TGKPG	TTINAD	GWANFSVNGGS
421	-NSCLAV	VLVTNGD	QGWK	HEVGEI	YAGKTF	VDYLG	NCQE	QVVGID	GDGDFVESAS
482	WVKR	485							
		:							
480	WVPK	483							
		:							

Search completed: October 7, 2004, 00:18:55  
Job time : 47.501 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.886 Seconds  
(without alignments)  
3134.012 Million cell updates/sec

Title: US-09-925-576C-4  
Perfect score: 2720  
Sequence: 1 HHNGTGTMMQYFEWHLPNL.....ADGMANFVNGSGSVIWKVR 485  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2414	88.8	518	1 A27705	alpha-amylase (EC
2	1947	71.6	512	1 ALBSL	alpha-amylase (EC
3	1888.5	69.4	549	1 A24549	alpha-amylase (EC
4	1887.5	69.4	549	1 A54541	alpha-amylase (EC
5	1880.5	69.1	549	1 A24436	alpha-amylase (EC
6	1871	68.8	514	1 ALBSN	alpha-amylase (EC
7	1816	66.8	548	1 ALBSF	alpha-amylase (EC
8	1373	50.5	493	2 S15713	alpha-amylase (EC
9	1267	46.6	484	2 G95160	alpha-amylase (imp
10	1265	46.5	484	2 F98026	alpha-amylase (EC
11	1245	45.8	492	2 AH2079	alpha-amylase (imp
12	1143	42.0	491	2 C86781	alpha-amylase (imp
13	1104	40.6	506	2 G98247	cytoplasmic alpha-
14	1103	40.6	495	2 AD3038	alpha-amylase amyA
15	1084	39.9	494	1 B45738	alpha-amylase (EC
16	1072	39.4	494	2 AD0751	cytoplasmic alpha-
17	1071	39.4	495	2 B90962	cytoplasmic alpha-
18	1064	39.1	495	1 A45738	alpha-amylase (EC
19	1052	38.7	495	2 B85810	cytoplasmic alpha-
20	379.5	14.0	217	2 A19506	alpha-amylase (EC
21	327	12.0	1196	2 A29130	beta-amylase (EC 3
22	322.5	11.9	482	2 S31478	alpha-amylase (EC
23	301.5	11.1	421	2 S10514	alpha-amylase (EC
24	288	10.6	423	2 T09942	alpha-amylase (EC
25	274.5	10.1	440	2 S14958	alpha-amylase (EC
26	271	10.0	428	2 T05521	alpha-amylase (EC
27	271	10.0	504	2 A55861	alpha-amylase (EC
28	269	9.9	826	2 E96720	probable alpha-amyl
29	268.5	9.9	547	2 A32803	glucan 1,4-alpha-m

RESULT 1

A27705

alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.  
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase  
C;Species: Bacillus sp.  
C;Date: 31-Mar-1989 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
C;Accession: A27705  
R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.  
Biochem. Biophys. Res. Commun. 151, 25-31, 1988

A;Title: Nucleotide sequence of the maltotetraose-producing amylase gene from an alkalophilic bacterium, *Halobacterium salinarum* R1.  
A;Reference number: A27705; MUID:88162814; PMID:3258152  
A;Accession: A27705  
A;Molecule type: DNA  
A;Residues: 1-518 <TSU>  
A;Cross-references: GB:M18862; NID:g142496; PID:AAA22231.1; PID:g142497  
A;Experimental source: chromosomal DNA of strain 707  
A;Note: amino end of mature protein also determined  
C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;34-518/Product: alpha-amylase #status experimental <MAT>  
F;236-369/Domain: alpha-amylase core homology <AMY>  
F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted  
F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 88.8%; Score 2414; DB 1; Length 518;  
Best Local Similarity 86.2%; Pred. No. 2.4e-157;  
Matches 418; Conservative 33; Mismatches 34; Indels 0; Gaps 0;

Qy	1	HHNGTGTMMQYFEWHLPNLDDASNLNRNRGITAIIWIPPAWKQTSQNDVGYGA	60
Db	34	HHNGTGTMMQYFEWHLPNLDDASNLNRNRGITAIIWIPPAWKQTSQNDVGYGA	93
Qy	61	YDYLDELGEFQKQVTRTKYGRSQLESIAIHALKNGVQVYGVVVMNHKGGADATENVLAV	120
Db	94	YDYLDELGEFQKQVTRTKYGRSQLESIAIHALKNGVQVYGVVVMNHKGGADATENVRAV	153
Qy	121	EVNPNRNRQELSGDYTTTEATWKFPDGRGNTYSDFKRWTHFDGVDVDSQSFQNRYYKF	180
Db	154	EVNPNRNRQELSGDYTTTEATWKFPDGRGNTYSDFKRWTHFDGVDVDSQSFQNRYYKF	213
Qy	181	RGDKKAWDEVDSENGYDYLMDADVDMDHPEVNVNELRWGEVYNTNTNLIDGFRIDAVKH	240
Db	214	RGDKKAWDEVDSENGYDYLMDADVDMDHPEVNVNELRWGEVYNTNTNLIDGFRIDAVKH	273
Qy	241	IKYSFTFDLWLTNRNATGKEMFAVAEFKNDLGALENLYLNTNNHSHSVDFVPLHNLNA	300
Db	274	IKYSFTFDLWLTNRNATGKEMFAVAEFKNDLGALENLYLNTNNHSHSVDFVPLHNLNA	333





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Db 390 VFTGDMYGTGDSQREIPALKKHKEPILKARKQVAYGAQHDYFPHHDIVGWTRREGDSVA 449
QY 423 NSGLATIMSDPGGCKMYGKQKAGQVHDDITGKPGKTTVINADGWANFVSGSVSIW 482
Db 450 NSGLAALITDGGCKMYGKQKAGQVHDDITGKPGKTTVINADGWANFVSGSVSIW 509
QY 483 VKR 485
Db 510 VQR 512

RESULT 3
A24549
Alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24549; I39501; I39770
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: A24549
A;Molecule type: DNA
A;Residues: 1-549 <GRA>
A;Cross-references: GB:M13255; NID:g142512; PID:AAA22241.1; PID:g142513
A;Experimental source: Genomic DNA of strain NZ-3
R;Satoh, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A;Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distant strains of Bacillus stearothermophilus
A;Reference number: I39501; MUID:88139156; PMID:3257753
A;Accession: I39501
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RES>
A;Cross-references: GB:M29577; NID:g142476; PID:AAA22225.1; PID:g142478
A;Experimental source: strain DY-5
A;Accession: I39770
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RE2>
A;Cross-references: GB:M29578; NID:g142484; PID:AAA22228.1; PID:g142486
A;Experimental source: strain 799
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.4%; Score 1888.5; DB 1; Length 549;
Best Local Similarity 67.7%; Pred. No. 2e-121;
Matches 325; Conservative 74; Mismatches 80; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLNDGNHNRRLRDDASNLNRGTTATWIPPAWKGTSQNDVGYGAYDLYD 65
Db 39 NGTMMQYFEWHLNDGNHNRRLRDDASNLNRGTTATWIPPAWKGTSQNDVGYGAYDLYD 98
QY 66 LGFENQKGTVRTKGTGTRSQLESALHAKNNGVQVYGVDMVNMHKGADATENVLAVEVNP 125
Db 99 LGFENQKGTVRTKGTGTRSQLESALHAKNNGVQVYGVDMVNMHKGADATENVLAVEVNP 158
QY 126 NRNEISGDYITAEATWTKDFPGRGNTYSDFKRWYHFDGVDWDSQROFQNRRIYKFRGDGK 185
Db 159 DRNQEISGTQIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217

RESULT 4
A54541
Alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI792)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C;Accession: A54541
R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A;Reference number: A54541
A;Accession: A54541
A;Molecule type: DNA
A;Residues: 1-549 <JOR>
A;Cross-references: GB:X59476
A;Experimental source: Chromosomal DNA of strain DNI792
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.4%; Score 1887.5; DB 1; Length 549;
Best Local Similarity 67.5%; Pred. No. 2.4e-121;
Matches 324; Conservative 74; Mismatches 81; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLNDGNHNRRLRDDASNLNRGTTATWIPPAWKGTSQNDVGYGAYDLYD 65
Db 39 NGTMMQYFEWHLNDGNHNRRLRDDASNLNRGTTATWIPPAWKGTSQNDVGYGAYDLYD 98
QY 66 LGFENQKGTVRTKGTGTRSQLESALHAKNNGVQVYGVDMVNMHKGADATENVLAVEVNP 125
Db 99 LGFENQKGTVRTKGTGTRSQLESALHAKNNGVQVYGVDMVNMHKGADATENVLAVEVNP 158
QY 126 NRNEISGDYITAEATWTKDFPGRGNTYSDFKRWYHFDGVDWDSQROFQNRRIYKFRGDGK 185
Db 159 DRNQEISGTQIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
QY 186 ANDWEVDSENGNDYLYMYADVMDHDPVNLRWGEMWYNTNLNLDGFRIDAVKHKYSF 245
Db 218 ANDWEVDSENGNDYLYMYADVMDHDPVNLRWGEMWYNTNLNLDGFRIDAVKHKYSF 277
QY 246 TRDWLTHVRNATGKEMFAVAFWKNLGALENLKNKNHNSVDFVPLHYNLYNASSGG 305
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QY 186 ANDWEVDSENGNDYLYMYADVMDHDPVNLRWGEMWYNTNLNLDGFRIDAVKHKYSF 245
Db 218 ANDWEVDSENGNDYLYMYADVMDHDPVNLRWGEMWYNTNLNLDGFRIDAVKHKYSF 277
QY 246 TRDWLTHVRNATGKEMFAVAFWKNLGALENLKNKNHNSVDFVPLHYNLYNASSGG 305
Db 278 FPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNITKTNGTMSLFDAPLHNKFTYASSGG 337
QY 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGSELESFVQEWFKPLAYALILTREQGYPS 365
Db 338 AFDMSTLMMNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWPKFLAYAFILTRQEGYPC 397
QY 366 VFTGDDYIGTFHSPVAMKAKIDPILKARQNFAYGTQHDYFDHNIICWTREGNTHPNSG 425
Db 398 VFYGDYIGTFHSPVAMKAKIDPILKARQNFAYGTQHDYFDHNIICWTREGNTHPNSG 457
QY 426 LATIMSDPGGCKMYGKQKAGQVHDDITGKPGKTTVINADGWANFVSGSVSIWVKR 485
Db 458 LAALITDGGCKMYGKQKAGQVHDDITGKPGKTTVINADGWANFVSGSVSIWVKR 517

RESULT 4
A54541
Alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI792)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C;Accession: A54541
R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A;Reference number: A54541
A;Accession: A54541
A;Molecule type: DNA
A;Residues: 1-549 <JOR>
A;Cross-references: GB:X59476
A;Experimental source: Chromosomal DNA of strain DNI792
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.4%; Score 1887.5; DB 1; Length 549;
Best Local Similarity 67.5%; Pred. No. 2.4e-121;
Matches 324; Conservative 74; Mismatches 81; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLNDGNHNRRLRDDASNLNRGTTATWIPPAWKGTSQNDVGYGAYDLYD 65
Db 39 NGTMMQYFEWHLNDGNHNRRLRDDASNLNRGTTATWIPPAWKGTSQNDVGYGAYDLYD 98
QY 66 LGFENQKGTVRTKGTGTRSQLESALHAKNNGVQVYGVDMVNMHKGADATENVLAVEVNP 125
Db 99 LGFENQKGTVRTKGTGTRSQLESALHAKNNGVQVYGVDMVNMHKGADATENVLAVEVNP 158
QY 126 NRNEISGDYITAEATWTKDFPGRGNTYSDFKRWYHFDGVDWDSQROFQNRRIYKFRGDGK 185
Db 159 DRNQEISGTQIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
QY 186 ANDWEVDSENGNDYLYMYADVMDHDPVNLRWGEMWYNTNLNLDGFRIDAVKHKYSF 245
Db 218 ANDWEVDSENGNDYLYMYADVMDHDPVNLRWGEMWYNTNLNLDGFRIDAVKHKYSF 277
QY 246 TRDWLTHVRNATGKEMFAVAFWKNLGALENLKNKNHNSVDFVPLHYNLYNASSGG 305
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[illegible]

Db	218	AWDWEVDTENGNYDLYMAYADLMDHPPEVUTELSKGKMYVNTTNDGFLDLAVKHKFSF	277
Qy	246	TRDWLTFRVNRATGKEMFAVAFWKNDLGALENLYNKTWNHVSFVDVPLHYNLYNASNSGG	305
Db	278	FPDWLSVRSQTGKPLFTVIGYVSWDINKLHNYINKTGTMSLFDAPLHNKFTASKSGG	337
Qy	306	NYDMAKLNGTVQVKQPMHVAVTFVDNHDSDQPEESLESFVQEWFKPLAYALILTRREGGYPS	365
Db	338	TFDMRTLMTNLMDKQDPTLAVTFVDNHDTEPQALQSWVDPMFKPLAYAFILTRQEGYPC	397
Qy	366	VFYGDYVIGIPHSPVAMKAKIDPILAEARONFAYGTOHDYFDHNNIIGWTRGNTHTPNSG	425
Db	398	VFYGDYVIGIPQYNTPSLKSIDPLLIARRDYAYGTOHDYLDHSDIIGWTRGVTETKPGSG	457
Qy	426	LATIMSDPGGCKWMYGVQNKAGOVWHIDITGNKPGTIVTINADGWANFVSNGGVSIVWVKR	485
Db	458	LALITDPPGSKWMYGVQKHAGKVFDLTGNRSVTIINSNGWGEFKVNGGVSIVWVPR	517

RESULT 6

ALSN

alpha-amylase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Bacillus amyloliquefaciens

C/Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #text\_change 18-Jun-1999

C/Accession: A92389; A90307; I39763; I39763; A00843

R/Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L. J. Biol. Chem. 259, 1007-1013, 1983

A/Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced fr

A/Reference number: A92389; MUID:83108808; PMID:6185474

A/Contents: pUB110

A/Accession: A92389

A/Molecule type: DNA

A/Residues: 1-514 <TAK>

A/Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA22121

R/Chung, H.S.; Friedberg, F. Biochem. J. 185, 387-395, 1980

A/Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase.

A/Reference number: A90307; MUID:80241725; PMID:6156671

A/Accession: A90307

A/Molecule type: protein

A/Residues: 32-53,'I','55-63','L','65-78','D','80-83','S','85-222 <CHU>

R/Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.; Gene 15, 43-51, 1981

A/Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of th

A/Reference number: I39756; MUID:82051296; PMID:6170539

A/Accession: I39756

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-96 <RES>

A/Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298

R/Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S. Gene 59, 161-170, 1987

A/Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells by its own

A/Reference number: I39763; MUID:88137952; PMID:2830166

A/Accession: I39763

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-39 <RES2>

A/Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F/1-31/Domain: signal sequence #status predicted <SIG>

F/32-514/Product: alpha-amylase #status predicted <MPT>

F/229-362/Domain: alpha-amylase core homology <AMY>

F/133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted

F/262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 68.8%; Score 1871; DB 1; Length 514;



QY 6 NGTMMQYFEWHLFNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLYD 65  
Db 4 NHTMMQYFEWHLAAGDGHKRLAEMAPELKAGIDTVMVPVTKAVSAEDTGGVGYDLYD 63  
QY 66 LGFENQKGTVRTKYGTRSQLESIAHALKNNGVQYGVVNMHKGADATENVLAVENPN 125  
Db 64 LGFEDQKGTVRTKYGTRKQELIEIAECQKNGIAVYVLDVNMHKGADETEVFKVIEDPN 123  
QY 126 NRQIEISGDTYIEAWTKDFPFGRGNTYSDFKRWYHFDGVDWQSRQFNRIYKFRGDGK 185  
Db 124 DRTKEISEPFEIEGWTKTFPGRGQYSSPKWSEHFNQDFD-AREERTGVFRIAGENK 182  
QY 186 AWDWEVDSENGNDYLMYADVMDHDPVNVNLRWGEWYNTNLNDGFRIDAVKHICYSP 245  
Db 183 KWNENVDENGDYLMYANFNDYHDPVRREMDWGWKLIDTLQCGFRDLDAIKHINHEF 242  
QY 246 TRDWLTHVRNATKEMFAVAEFWKNDLGALENLYNKTNWNHSDVDFPLHYNLYNASNG 305  
Db 243 IKFEFAEMIRKRQGFYIVGFEFWNSLDA CREFLDTVDYQIDFLDVSFLHYKLHEASLKR 302  
QY 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEWFKPLAYALILFREOGYPS 365  
Db 303 DFDLSKIFDITLQVTHAVTFVDNHDSPHEALESWIGDWFKPSAYALTLLRRDGPV 362  
QY 366 VFYGDYIGI-PTHSVPAWKAKIDPILFARONFAYGTHQDHYFDHNNIGWTRGNTTHPS 424  
Db 363 VFYGDYIGIGPFPVQKKEILAILLSARCNKAYGEQDYFDHANTIGWVRGVBEIEGS 422  
QY 425 GLATIMSDGPGGKMWYVQKQAGOVWHDTGNKPGTVTINADGMANFVNGSGSVI 482  
Db 423 GCAVVISGDDGKRMFIGEHRAGEVWVDLTKSCDDQITIEEDGMATFHVCGGGSVW 480

RESULT 9  
G95160  
alpha-amylase [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
C:Accession: G95160  
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: G95160  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-484 <KUR>  
A:Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4  
A:Experimental source: strain TIGR4  
C:Genetics:  
C:Gene: Spi382  
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 46.6%; Score 1267; DB 2; Length 484;  
Best Local Similarity 49.0%; Pred. No. 4.9e-79;  
Matches 235; Conservative 77; Mismatches 162; Indels 6; Gaps 4;

QY 6 NGTMMQYFEWHLFNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLYD 65  
Db 3 NQTLAQYFEWYLPDGHQWTRLAENAPHLAHLGISHVWMPAPKATNEKXDVGVGYDLYD 62  
QY 66 LGFENQKGTVRTKYGTRSQLESIAHALKNNGVQYGVVNMHKGADATENVLAVENPN 125  
Db 63 LGFENQKGTVRTKYGFKEDYLQAIQALKAQGIQPMADVVLNHNKAAADHREAFQVIEVDV 122  
QY 126 NRQIEISGDTYIEAWTKDFPFGRGNTYSDFKRWYHFDGVDWQSRQFNRIYKFRGDGK 185  
Db 123 DRTVGEPEPTINGWTSFTFDGQDYNGFHHWHFTGTDYDAKRS-KSGIYLQGDNK 181  
QY 186 AWDWE--VDSENGNDYLMYADVMDHDPVNVNLRWGEWYNTNLNDGFRIDAVKHICY 245  
Db 183 KWNENVDENGDYLMYANFNDYHDPVRREMDWGWKLIDTLQCGFRDLDAIKHINHEF 242  
QY 246 TRDWLTHVRNATKEMFAVAEFWKNDLGALENLYNKTNWNHSDVDFPLHYNLYNASNG 305  
Db 243 IKFEFAEMIRKRQGFYIVGFEFWNSLDA CREFLDTVDYQIDFLDVSFLHYKLHEASLKR 302  
QY 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEWFKPLAYALILFREOGYPS 365  
Db 303 DFDLSKIFDITLQVTHAVTFVDNHDSPHEALESWIGDWFKPSAYALTLLRRDGPV 362  
QY 366 VFYGDYIGI-PTHSVPAWKAKIDPILFARONFAYGTHQDHYFDHNNIGWTRGNTTHPS 424  
Db 363 VFYGDYIGIGPFPVQKKEILAILLSARCNKAYGEQDYFDHANTIGWVRGVBEIEGS 422  
QY 425 GLATIMSDGPGGKMWYVQKQAGOVWHDTGNKPGTVTINADGMANFVNGSGSVI 482  
Db 423 GCAVVISGDDGKRMFIGEHRAGEVWVDLTKSCDDQITIEEDGMATFHVCGGGSVW 480

Db 182 GWANEELVDNENGYDLYMAYADLDFKHPEVIQNIYDWMDFMETTGTGAGFLDAVRKIDS 241  
QY 244 SFTRDWLTHVRNATKEMFAVAEFWKNDLGALENLYNKTNWNHSDVDFPLHYNLYNASNG 303  
Db 242 FPMRNFIRDMKEKYGDDFVFGFENPDKEANUDYLEKTEEHFDLVDVRLHQLNFEASQA 301  
QY 304 GGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEWFKPLAYALILFREOGY 363  
Db 302 GANYDLRGIFTDSLVELKPKAVTFVDNHDTRQGALESTVEEWFKPAAYALILLRQDGL 361  
QY 364 PSVFGDYIGIP-THSVPAWKAKIDPILFARONFAYGTHQDHYFDHNNIGWTRGNTTHP 422  
Db 362 PCVFGDYIGISQYQAQEDFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSG--AEN 419  
QY 423 NSGLATIMSDGPGGKMWYVQKQAGOVWHDTGNKPGTVTINADGMANFVNGSGSVI 482  
Db 420 QSPIAVLISNDQENSKSMFVQEWNTQTTFVDLLGNHQGVTTIDEEGYQFPVSARSVSW 479

RESULT 10  
F98026  
alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 02-Nov-2001  
C:Accession: F98026  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: F98026  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-484 <KUR>  
A:Cross-references: GB:AE007317; PIDN:AAAL00043.1; PID:g15458876; GSPDB:GN00174  
C:Genetics:  
C:Gene: amy  
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
C:Keywords: glycosidase; hydrolase

Query Match 46.5%; Score 1265; DB 2; Length 484;  
Best Local Similarity 48.8%; Pred. No. 6.7e-79;  
Matches 234; Conservative 79; Mismatches 161; Indels 6; Gaps 4;

QY 6 NGTMMQYFEWHLFNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLYD 65  
Db 3 NQTLAQYFEWYLPDGHQWTRLAENAPHLAHLGISHVWMPAPKATNEKXDVGVGYDLYD 62  
QY 66 LGFENQKGTVRTKYGTRSQLESIAHALKNNGVQYGVVNMHKGADATENVLAVENPN 125  
Db 63 LGFENQKGTVRTKYGFKEDYLQAIQALKAQGIQPMADVVLNHNKAAADHREAFQVIEVDV 122  
QY 126 NRQIEISGDTYIEAWTKDFPFGRGNTYSDFKRWYHFDGVDWQSRQFNRIYKFRGDGK 185  
Db 123 DRTVGEPEPTINGWTSFTFDGQDYNGFHHWHFTGTDYDAKRS-KSGIYLQGDNK 181  
QY 186 AWDWE--VDSENGNDYLMYADVMDHDPVNVNLRWGEWYNTNLNDGFRIDAVKHICY 243  
Db 182 GWANEELVDNENGYDLYMAYADLDFKHPEVIQNIYDWMDFMETTGTGAGFLDAVRKIDS 241  
QY 244 SFTRDWLTHVRNATKEMFAVAEFWKNDLGALENLYNKTNWNHSDVDFPLHYNLYNASNG 303  
Db 242 FPMRNFIRDMKEKYGDDFVFGFENPDKEANUDYLEKTEEHFDLVDVRLHQLNFEASQA 301  
QY 304 GGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEWFKPLAYALILFREOGY 363  
Db 302 GANYDLRGIFTDSLVELKPKAVTFVDNHDTRQGALESTVEEWFKPAAYALILLRQDGL 361  
QY 364 PSVFGDYIGIP-THSVPAWKAKIDPILFARONFAYGTHQDHYFDHNNIGWTRGNTTHP 422

Db 362 PCVFYGYGYSQYAOQDPKEILDRLLAIRKDLAYGEQNDYFPHANCIGWVRSG--AEN 419  
Qy 423 NSGLATIMSDPGGKWMYQGNKAGQVWHIDITGNKPGTVTINADGWANFVNGSVSIW 482  
Db 420 QSPIAVLISNDQENSKSMFVQEWNTQTFVDLLGSHQGVITDEBGYQGPVFSARSVSW 479  
RESULT 11  
AH2079  
alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C;Accession: AH2079  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AH2079  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-492 <KUR>  
A;Cross-references: GB:BA000019; PIDN:BA073889.1; PID:g17131281; GSPDB:GN00179  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr2190  
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 45.8%; Score 1245; DB 2; Length 492;  
Best Local Similarity 48.1%; Pred. No. 1.6e-77;  
Matches 236; Conservative 84; Mismatches 155; Indels 16; Gaps 5;  
Qy 6 NGTMQYFEWHLPNDCNHNRLRDDASNLNRGITAIPPAWKGTSON-DVGYGAYDLY 64  
Db 5 NGTMQYFHWIIPNDGNLNSKVSASAPELADAGTAMWLPPAYKGFAGSDVGVGYDLY 64  
Qy 65 DLGEFNGKGTVRTKYGTRSQLESIAHALKXNGVQVGVYVNMHKGADATENVLAVEVNP 124  
Db 65 DLGEFDQKGSVRTKYGTRQYLDVAVKSLQTHGLQVYADAVLNHKGWDGAVETPKATPPQ 124  
Qy 125 NNRNQEISGDIYIEAWTKFDPGRGNTYSDPKRWYHFDGVWDQSQFQNRIFYKRGDG 184  
Db 125 DRLNPKGGLQDIKTYTHYFPPGRQGYKSNPEWHWHFDDAVDYNEYS-GDRSTVYLLE 183  
Qy 185 KANDWEVDSNGYDLYMADVMDHPVNNELRWGEWYTNLNLGFRIDAVKHIKYS 244  
Db 184 KNFDYVALEKGFAYLWGCDDLDPQNEWVRGEVTVYWKWCLDTTKVDGFRIDAIKHISTW 243  
Qy 245 FTRDLWTHVRNATGKEMPAFAEFKNDLGALENLNTNWNHVSFVDFPLHNLNYSNNG 304  
Db 244 FFPWIDALERHAGKDLFMVGEYWNIDNTLLWTVDAVRGMSVDFVPLHNFHQAQSKG 303  
Qy 305 GNYDMAKLLNGTVVQKHPHIAVTFVDNHDSPQGSLESFVQEWFKPLAYALILTRQGY 364  
Db 304 GNYDMRRLDGTMMQRPHTAVTFVENHDSPLQALSVBEPFKPLAYAILLRKQGY 363  
Qy 365 SVFQYGYGTPHS-----VPAMKAKIDPILAEARONFAYGTOHDYFDHNNIGW 413  
Db 364 CVFHADYTGAEYEDWGDGRNRYNIFMPSHRWIIDKLAYARKHYAGPQYNLYDHWNTIGW 423  
Qy 414 TREGNTTHPSGLATIMSDGPGKWMYVQGNKAGQVWHIDITGNKPGTVTINADGWANF 473  
Db 424 TRLGDAHP-OGMAVIMSDSGEGIKWMEVG--KNTKPIDUTEHKEAVYTNWGWGEFR 480  
Qy 474 VNGGSVSIWK 484  
Db 481 CLGGSVSVWQ 491

RESULT 12  
C86781  
alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C;Accession: C86781  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich,  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: C86781  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-491 <STO>  
A;Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: amyL  
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 42.0%; Score 1143; DB 2; Length 491;  
Best Local Similarity 42.8%; Pred. No. 1.5e-70;  
Matches 205; Conservative 104; Mismatches 166; Indels 4; Gaps 3;  
Qy 8 TMQYFEWHLPNDCNHNRLRDDASNLNRGITAIPPAWKGTSON-DVGYGAYDLYDL 66  
Db 3 TIIQAFWYLPSSQHNWNIKENIPDLKLGFLPSGLWLPASKASGVEDVGYGYDLYDL 62  
Qy 67 GEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVGVYVNMHKGADATENVLAVEVNP 126  
Db 63 GEFQKGTIPTKYGTRKDEYLDLINTLHNNIEVYADIVFNHMGADTETIADIKAE 122  
Qy 127 RNRNQEISGDIYIEAWTKFDPGRGNTYSDPKRWYHFDGVWDQSQFQNRIFYKRGDGA 186  
Db 123 HLHNIENKKTVEWTKFTFFPGRQGYDNYITWNHFTGIDYDE-RKNQEBILEF--EGHE 179  
Qy 187 WDNEVDSNGYDLYMADVMDHPVNNELRWGEWYTNLNLGFRIDAVKHIKYSFT 246  
Db 180 WDNEVDSNNFYLMDGADLDFSVSEIVQEKWGHFWSEWTKIDGFRIDAIDPKYF 239  
Qy 247 RDMLTVRNATGKEMPAFAEFKNDLGALENLNTNWNHVSFVDFPLHNLNYSNNG 306  
Db 240 DKWLEQRAKDLRKLFTVGEVWSDDLKLEYLEQSSDRQLQFDVPLHFNKKEASTNGE 299  
Qy 307 YDMAKLLNGTVVQKHPHIAVTFVDNHDSPQGSLESFVQEWFKPLAYALILTRQGY 366  
Db 300 FDMRTLFDHTLTASQPELSVTFVDNHDTPQEQALQSWIPAWFKHAYSLILRRKKTPT 359  
Qy 367 FYGDIYGYTPHSVPAMKAKIDPILAEARONFAYGTOHDYFDHNNIGTREGNTTHPS 426  
Db 360 FWGLYGIPTSHNPNVPGDNLRTMIALRKSEFLRENDYFDHPDILIGWNTILKIDNKEY 419  
Qy 427 ATMSDGPGEKWMYVQGNKAGQVWHIDITGNKPGTVTINADGWANFVNGGSVSIWK 485  
Db 420 SCILTNKNGSKYMIIDKAYAGVYIDLFGHHEIPTILDQNGGAFFVNDGVSVMVDK 478  
RESULT 13  
G98247  
cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacteri  
C;Species: Agrobacterium tumefaciens  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002  
C;Accession: G98247  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A;Reference number: A97359; MUID:21608551; PMID:11743194  
A;Accession: G98247  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-506 <KUR>  
A;Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170  
C;Genetics:  
A;Gene: AGR\_L1863  
A;Map position: linear chromosome

C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 40.6%; Score 1104; DB 2; Length 506;  
Best Local Similarity 44.0%; Pred. No. 7e-68;  
Matches 218; Conservative 83; Mismatches 176; Indels 18; Gaps 6;

QY 3 NGTNGTMMQYFEWHLPNQGNHNRRLDDASNLNRNGITAIWIPPAWKGTSON-DVGYGAY 61  
DB 11 NMAGRTLLQFFHWYPPDGGKLMSEVAEKAESLAKMGITDVLPPAVKGAAGGYSVGYDTY 70  
QY 62 DLYDLGFGNOKGTVTKYGRSQALESIAHLKNGGVQVGVVNNHKGADATENVLAVE 121  
DB 71 DLFDLGFGDQKGVATKYGRALAEHAGKTLKONGIRVHDDVNLNHHKGADEKEKVRVR 130  
QY 122 VFNPNRNOEISGDYTIETAWTKFPFGRGNTYSDFKRWYHFDGVDM--DQSRQFQNRYYK 179  
DB 131 VNPDRDIDDEPPALAYTRFTFPGNGKHSKEIWLKCFSGVDHIEEPTDGIIFRLVN 190  
QY 180 FRDQKAWDEVDSENGNYDLYMADVMDHPVNNELRWGEWYNTNLNLDGFRIDAVK 239  
DB 191 EYGDGE-WNEEVDQENGNYDLYMADVMDHPVNNELRWGEWYNTNLNLDGFRIDAVK 249  
QY 240 HIKYSFTRDLWTRNATGKEMFAEFAEFKNDLGALENLNTNNHNSVDFVPLHYNLYN 299  
DB 250 HIFAWFRDVGWHRETVDPLFVVAEYHHPDLLEALKSYLELYDKQLMLFDVALHHSFHD 309  
QY 300 ASNSGGNYDMKLLNGTVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTR 359  
DB 310 ASKQGGDFMRSIFDGLSVSAVDPHATVLDNHDTPQLSLEAPVFPWFKPLAYAILLR 369  
QY 360 EQGYSVYFGDYGYIP-----THSVPAWMAKIDIPLEARNQFAYGTQHDYFDHH 408  
DB 370 EEGVPCVFPDLFGTSYTDGTGNGNEYKIDIPATEC-LPKLIEARSRFANGPQTDIFDDA 428  
QY 409 NIIGTWREGNTHPNGLATIMSDGPGGKMWYGVQNKAGOVVHDTGNKPGTWTINADG 468  
DB 429 SCIAFIRHGTADAP--GCVVVMSNGEPGEKQADLGPERRAGSVWRDFLGHRREHITLDES 486  
QY 469 WANFSVNGGSVSIWV 483  
DB 487 KGTFTFNGGSVSVWV 501

RESULT 14  
AD3038

A:alpha-amylase amYA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AD3038  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; PMID:21608550; PMID:11743193

A:Accession: AD3038  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-495 <KUR>

A:Cross-references: GB:AE008689; PIDN:AAI44722.1; PID:gl7742354; GSPDB:GN00187  
A:Experimental source: strain C58 (Dupont)

C:Genetics:  
A:Gene: amYA

A:Map position: linear chromosome  
C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 40.6%; Score 1103; DB 2; Length 495;  
Best Local Similarity 44.3%; Pred. No. 8e-68;  
Matches 217; Conservative 83; Mismatches 172; Indels 18; Gaps 6;

QY 8 TMMQYFEWHLPNQGNHNRRLDDASNLNRNGITAIWIPPAWKGTSON-DVGYGAYDLYL 66

DB 5 TLLQFFHWYPPDGGKLMSEVAEKAESLAKMGITDVLPPAVKGAAGGYSVGYDTYDLFDL 64  
QY 67 GFENOKGTVTKYGRSQALESIAHLKNGGVQVGVVNNHKGADATENVLAVEVNPNN 126  
DB 65 GEPDQKGVATKYGRALAEHAGKTLKONGIRVHDDVNLNHHKGADEKEKVRVRVNPDD 124  
QY 127 RNOEISGDYTIETAWTKFPFGRGNTYSDFKRWYHFDGVDM--DQSRQFQNRYYKFRGDG 184  
DB 125 RTDIDDEDPPALAYTRFTFPGNGKHSKEIWLKCFSGVDHIEEPTDGIIFRLVNEVG 184  
QY 185 KAWDEVDSENGNYDLYMADVMDHPVNNELRWGEWYNTNLNLDGFRIDAVKIKYS 244  
DB 185 E-WNEEVDQENGNYDLYMADVMDHPVNNELRWGEWYNTNLNLDGFRIDAVKIPAW 243  
QY 245 FTRDLWTRNATGKEMFAEFAEFKNDLGALENLNTNNHNSVDFVPLHYNLYNASNG 304  
DB 244 FRDQKAWDEVDSENGNYDLYMADVMDHPVNNELRWGEWYNTNLNLDGFRIDAVKIKYS 303  
QY 305 GNYDMAKLLNGTVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTREQGY 364  
DB 304 GDFMRSIFDGLSVSAVDPHATVLDNHDTPQLSLEAPVFPWFKPLAYAILLR 363  
QY 365 SVFYGDYGYIP-----THSVPAWMAKIDIPLEARNQFAYGTQHDYFDHHIIGW 413  
DB 364 CVFYPDLPFGTSYTDGTGNGNEYKIDIPATEC-LPKLIEARSRFANGPQTDIFDDASCI 422  
QY 414 TREGNTHPNGLATIMSDGPGGKMWYGVQNKAGOVVHDTGNKPGTWTINADGWANFS 473  
DB 423 IRHGTADAP--GCVVVMSNGEPGEKQADLGPERRAGSVWRDFLGHRREHITLDES 480  
QY 474 VNGGSVSIWV 483  
DB 481 TNGGSVSVWV 490

RESULT 15

B45738

A:alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium  
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C:Species: Salmonella typhimurium

C:Date: 07-Apr-1994 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
C:Accession: B45738

R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.  
J. Bacteriol. 174, 6644-6652, 1992

A:Title: Escherichia coli produces a cytoplasmic alpha-amylase, amYA.  
A:Reference number: A45738; PMID:9301517; PMID:1400215

A:Accession: B45738  
A:Molecule type: DNA

A:Residues: 1-494 <RAH>  
A:Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045

C:Genetics:  
A:Gene: amYA

C:Function:  
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation  
C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C:Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation  
F:202-335/Domain: alpha-amylase core homology <AMY>

F:239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.9%; Score 1084; DB 1; Length 494;  
Best Local Similarity 42.5%; Pred. No. 1.6e-66;  
Matches 209; Conservative 83; Mismatches 182; Indels 18; Gaps 6;

QY 6 NCTMMQYFEWHLPNQGNHNRRLDDASNLNRNGITAIWIPPAWKGTSON-DVGYGAYDLY 64

DB 3 NPTLLQYFHWYPPDGGKLMSELAERADGLNDGINMVLPPACKGASGYSVGYDTYDLF 62

QY 65 DLGEFNOKGTVTKYGRSQALESIAHLKNGGVQVGVVNNHKGADATENVLAVEVNP 124

DB 63 DLGEFNOKGTVTKYGRSQALESIAHLKNGGVQVGVVNNHKGADATENVLAVEVNP 122

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QY 125 NNRQETSGDYTTIEAWTKDFPPGRGNTYSDFKRWYHFDGVDMDQSQFQNRYYKFRGD- 183
Db 123 DDRTOIDNNIIECEGWTRYTFPARAGQYSNFINDYHCFSGIDHIENPD-EDGIFKIYNDY 181
QY 184 -GXAWDEVDSENGNDYLYADVDMDHPVNVNELRWGEWYTNLMDGFRIDAVKHK 242
Db 182 TGGMNDQVDDMGNFYDLNGENIDFRNHAVTEIYKWARVWMEQTHCDGFRLDVAVRHP 241
QY 243 YSFTRWLTHVRNATGKEMFAVAEFWKNDLGALENYLKNKNHNSVFDVPLHVNLYNASN 302
Db 242 AWFYKEWIEHVQAVAPKPLFIVAELWSHEVDKLTYYIDQVDGKTMLFDAPLOMKFHEASR 301
QY 303 SGGNYDMAKLLNGTVVQKHMPHIAVTFVDNHDQGESLESFVQEWFKPLAYALILTREQ 362
Db 302 QGAEDMRHIFTGTLVEADPFHATLVANHDTQPLQALEAPVEPWFKPLAYALILLRENG 361
QY 363 YPSVFYCDYIGIPH-----SVPAMKAKIDPILARQNPAYGTQHDYFDHNII 411
Db 362 VPSVFYDLYGASYEDSGENGETCRVDMFVIN-QLDRLLILARQRFHAGIQTLFFDHENCI 420
QY 412 GWTREGNTHPNGLATIMSDGPGGKRWYVQNKAGQVWHDITGNKPGTGTVTINADGMAN 471
Db 421 AFRSG--TEENPGCVVLSNGDDGKTLILGDNYANKTWDRDFSGNRDEYVVTNDQGEAT 478
QY 472 FSVNGGSVSIWV 483
Db 479 FFCNAGSVSVWV 490

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Search completed: October 7, 2004, 00:20:42  
Job time : 16.886 secs

***This Page Blank (uspto)***



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.50628 Seconds  
(without alignments)  
2968.867 Million cell updates/sec

Title: US-09-925-576C-4

Perfect score: 2720

Sequence: 1 HHNGTNGTMMQYFEWHLPLND.....ADGWANFVNGSGSVSIWVKR 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1.	2414	88.8	518	1 AMT6_BACS7	P19571 bacillus sp
2.	1947	71.6	512	1 AMY_BACLI	P06278 bacillus li
3.	1880.5	69.1	549	1 AMY_BACST	P06279 bacillus st
4.	1871	68.8	514	1 AMY_BACAM	P06692 bacillus am
5.	1082	39.8	494	1 AMY2_SALTY	P26613 salmonella
6.	1064	39.1	495	1 AMY2_ECOLI	P26612 escherichia
7.	327	12.0	1196	1 AMYB_PABPO	P21543 paenibacill
8.	301.5	11.1	421	1 AMYA_VIGMU	P17859 vigna mungo
9.	275	10.1	548	1 AMT4_PSEST	P13507 pseudomonas
10.	274.5	10.1	440	1 AM3A_ORYSA	P27932 oryza sativ
11.	264.5	9.7	435	1 AM3D_ORYSA	P27933 oryza sativ
12.	262.5	9.7	551	1 AMT4_PSESA	P22963 pseudomonas
13.	262	9.6	427	1 AMY2_HORVU	P04063 hordeum vul
14.	261	9.6	713	1 CDGT_BACS8	P17692 bacillus sp
15.	261	9.6	713	1 CDGT_BACS3	P09121 bacillus sp
16.	260	9.6	713	1 CDGT_BACS0	P05618 bacillus sp
17.	258.5	9.5	428	1 AMY1_ORYSA	P17654 oryza sativ
18.	258.5	9.5	719	1 AMYM_BACST	P19531 bacillus st
19.	258	9.5	368	1 AMY3_HORVU	P04747 hordeum vul
20.	256.5	9.4	498	1 AMYA_ASAPW	Q02905 aspergillus
21.	256.5	9.4	499	1 AMYB_ASAPW	Q02906 aspergillus
22.	254	9.3	437	1 AM3E_ORYSA	P27934 oryza sativ
23.	252.5	9.3	413	1 AMY3_WHEAT	P08117 triticum ae
24.	252.5	9.3	438	1 AMY1_HORVU	P00693 hordeum vul
25.	251.5	9.2	499	1 AMYA_ASPOP	P10529 aspergillus
26.	251	9.2	429	1 AMY6_HORVU	P04750 hordeum vul
27.	249	9.2	713	1 CDGT_BACSP	P30921 bacillus sp
28.	248.5	9.1	499	1 AMY_ASPSH	P20292 aspergillus
29.	248	9.1	438	1 AM3B_ORYSA	P27937 oryza sativ
30.	243	8.9	437	1 AM3C_ORYSA	P27939 oryza sativ
31.	243	8.9	703	1 CDGT_BACS2	P31746 bacillus sp
32.	243	8.9	710	1 CDGT_THETU	P26827 thermoanaer
33.	243	8.9	713	1 CDGU_BACCI	P43379 bacillus ci

## ALIGNMENTS

RESULT 1

ID	AMT6_BACS7	STANDARD;	PRT;	518 AA.
AC	P19571;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Glucan 1,4-alpha-maltohexaosidase precursor (SC 3.2.1.98) (G6-amyase)			
DE	(Maltose-6-phosphate-producing amylase) (Exo-maltohexaohydrolase).			
OS	Bacillus sp. (strain 707).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1416;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.			
RX	MEDLINE=88162814; PubMed=3258152;			
RA	Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;			
RT	"Nucleotide sequence of the maltose-6-phosphate-producing amylase gene from an alkalophilic Bacillus sp. #707 and structural similarity to liquefying type alpha-amyases.";			
RL	Biochem. Biophys. Res. Commun. 151:25-31(1988).			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylose polysaccharides so as to remove successive maltose residues from the non-reducing chain ends.			
CC	-1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By similarity).			
CC	-1- PATHWAY: Starch degradation.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL; M18862; AAA22231.1; ..			
DR	PIR; A27705; A27705.			
DR	HSP; P06278; 1VJ8.			
DR	InterPro; IPR006589; Alp_amy1_cat_sub.			
DR	InterPro; IPR006047; Alpha_amy1_cat.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF001128; alpha-amyase; 1.			
DR	PRINTS; PR00110; ALPHAMYLASE.			
DR	SMART; SM00642; Amy; 1. Carbohydrate metabolism; Signal.			
KW	Hydrolase; Glycosidase;			
FT	SIGNAL 1 33			
FT	CHAIN 34 518			
FT	ACT_SITE 269 269			
FT	BY SIMILARITY.			
FT	ACT_SITE 273 273			
FT	BY SIMILARITY.			
FT	ACT_SITE 366 366			
FT	BY SIMILARITY.			
FT	METAL 139 139			
FT	CALCIUM 1 (BY SIMILARITY).			
FT	CALCIUM 2 AND SODIUM (BY SIMILARITY).			
FT	METAL 196 196			
FT	CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).			
FT	METAL 219 219			

P08137 bacillus ci  
P21567 saccharomyc  
P30920 bacillus ci  
P31747 bacillus sp  
P31835 paenibacill  
P27935 oryza sativ  
P27937 bacillus st  
Q05884 streptomyc  
P27941 oryza sativ  
P14014 bacillus li  
P80099 thermotoga  
O86956 thermotoga

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FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT METAL 240 240 CALCIUM 2 (BY SIMILARITY).
FT METAL 242 242 CALCIUM 2 (BY SIMILARITY).
FT METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
  Query Match 88.8%; Score 2414; DB 1; Length 518;
  Best Local Similarity 86.2%; Pred. No. 1.4e-155;
  Matches 418; Conservative 33; Mismatches 34; Indels 0; Gaps 0;
QY 1 HHNGTGTMMQYFEWHLPLNDGNHWRNLRDASNLNRGITAIPPAWKGTQNDVGYGA 60
DB 34 HHNGTGTMMQYFEWHLPLNDGNHWRNLRDASNLKSGITAVIPPAWKASQNDVGYGA 93
QY 61 YDLYLGEFQKQKTVRTKYTRQSLQSAIAHLKKNQGVQYGVVVMNHKGGADATENVLAV 120
DB 94 YDLYLGEFQKQKTVRTKYTRQSLQAAVTSKNGGIQVYGVVVMNHKGGADATENVRAV 153
QY 121 EVNPNRNRQISGDYITIAWTKFDFGGRGNTYSDFKRWVHFDGVQDWDQSRQFNRIYKF 180
DB 154 EVNPNRNRQISGDYITIAWTKFDFGGRGNTYSDFKRWVHFDGVQDWDQSRQFNRIYKF 213
QY 181 RGDGKAWDWEVDSENGNDYLYMADVDMHPEVNVNELRWGEWYTNLTLDGFRIDAVKH 240
DB 214 RGHGKAWDWEVDSENGNDYLYMADVDMHPEVNVNELRWGVVYTNLTLDGFRIDAVKH 273
QY 241 IKYSFTRDMWTHVRNATGKEMPAVAFWPKNDLGALENYLNKTNWNSHVFDPVPLHYNLYNA 300
DB 274 IKYSFTRDMWTHVRNATGKEMPAVAFWPKNDLGALENYLNKTNWNSHVFDPVPLHYNLYNA 333
QY 301 SNSGGNYDMAKLTGTVQHPHATVFDVNDHDSQPCESELESFVQEFKPLAYALITRE 360
DB 334 SKSGGNYDMENITGTVQHPHATVFDVNDHDSQPCESELESFVQEFKPLAYALITRE 393
QY 361 QGYPSVFGYDYGIPTHSVPAKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRGNTT 420
DB 394 QGYPSVFGYDYGIPTHSVPAKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRGNTA 453
QY 421 HPNSGLATIMSDGPGKMYGVQNKAGQVWHITGKTPGTVTINADGWANFVNGGSVS 480
DB 454 HPNSGLATIMSDGAGGSKWVFGNRKAGQVWSDITGRTGTVTINADGWANFVNGGSVS 513
QY 481 IWYKR 485
DB 514 IWVWK 518
RESULT 2
AMY_BACLI STANDARD; PRT; 512 AA.
AC P06278; Q84171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (BLA).
GN AMYS OR AMYL.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 27811;
RX MEDLINE=86115694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
RA Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
RT amino acid sequences of three bacterial liquefying alpha-amylases
RT deduced from the DNA sequences."
```

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RL J. Biochem. 98:1147-1156(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=861195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Requadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Shahhoseini M., Ziaei A.A., Ghaemi N., Pourbabaee A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RN Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Orlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372(1984).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Laoid B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to
RT promoter-independent catabolite repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2435-2442(1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373(1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=2192788; PubMed=11997021;
RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
RT "Action pattern and subsite mapping of Bacillus licheniformis
RT alpha-amylase (BLA) with modified maltooligosaccharide substrates.";
RL FEBS Lett. 518:79-82(2002).
RN [8]
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RX STRAIN=ATCC 6598; PubMed=2394736;
RA Declerck N., Joyet P., Gaillardin C., Masson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15488(1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RX STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037(1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RX ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
AND GLU-365.
RP STRAIN=ATCC 6598;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057(2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RX STRAIN=ATCC 6598;
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RX MEDLINE=22622182; PubMed=12736372;  
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,  
RA Gaillardin C.;  
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and  
RT modulation of its stability over a 50 degrees C temperature range.";  
RN Protein Eng. 16:287-293(2003).  
RN [12]  
RP MUTAGENESIS OF TRP-292 AND VAL-315.  
RC STRAIN=ATCC 27811;  
RX MEDLINE=22797417; PubMed=12915728;  
RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;  
RT "Alpha-amylase from Bacillus licheniformis mutants near to the  
RT catalytic site: effects on hydrolytic and transglycosylation  
RT activity.";  
RN Protein Eng. 16:505-514(2003).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RC STRAIN=ATCC 27811;  
RX MEDLINE=95182462; PubMed=787175;  
RA Machius M., Wiegand G., Huber R.;  
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-  
RT amylase at 2.2-A resolution.";  
RN J. Mol. Biol. 246:545-559(1995).  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RX MEDLINE=98212915; PubMed=9551551;  
RA Machius M., Declerck N., Huber R., Wiegand G.;  
RT "Activation of Bacillus licheniformis alpha-amylase through a  
RT disorder-->order transition of the substrate-binding site mediated  
RT by a calcium-sodium-calcium metal triad.";  
RN Structure 6:281-292(1998).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.  
RX MEDLINE=20384196; PubMed=10924103;  
RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,  
RA Svendsen A., Borchert T.V., Baurer Z., Wilson K.S., Davies G.J.;  
RT "Structural analysis of a chimeric bacterial alpha-amylase.  
RT High-resolution analysis of native and ligand complexes.";  
RN Biochemistry 39:9099-9107(2000).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT  
RH62V/N219F/A238V/Q293S/N294Y.  
RC STRAIN=ATCC 6598;  
RX MEDLINE=22538505; PubMed=12540849;  
RA Machius M., Declerck N., Huber R., Wiegand G.;  
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through  
RT introduction of hydrophobic residues at the surface.";  
RN J. Biol. Chem. 278:11546-11553(2003).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
CC linkages in oligosaccharides and polysaccharides.  
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.  
CC -1- SUBUNIT: Monomer.  
CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature  
CC liquefaction of starch-containing mashes and in the detergent  
CC industry to remove starch. Sold under the name Termamyl by  
CC Novozymes.  
CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH  
CC values (up to pH 11) and at high temperatures (up to 100 degrees  
CC Celsius).  
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
CC  
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CC  
DR EMBL; X03236; CAA26981.1; -;  
DR EMBL; M38570; AAA22226.1; -;  
DR EMBL; M13256; AAA22240.1; -;  
DR EMBL; K01984; AAA22193.1; -;

DR EMBL; AF438149; AAO26743.1; -;  
DR EMBL; M26412; AAA22237.1; -;  
DR EMBL; A17930; CAA01355.1; -;  
DR PIR; A91997; ALES1.  
DR PDB; 1BL1; 23-MAR-99.  
DR PDB; 1BPL; 17-AUG-96.  
DR PDB; 1E3X; 21-JUN-01.  
DR PDB; 1E3Z; 24-JUN-03.  
DR PDB; 1E40; 21-JUN-01.  
DR PDB; 1E43; 21-JUN-01.  
DR PDB; 1O80; 03-APR-03.  
DR PDB; 1VJ5; 12-MAR-97.  
DR InterPro; IPR006589; Alp\_amyl\_cat\_sub.  
DR InterPro; IPR006047; Alpha\_amyl\_cat.  
DR InterPro; IPR006046; Glyco\_hydro\_13.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR PRINTS; PR00110; ALPHAAMYLASE.  
DR SMART; SM00642; Amy; 1.  
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
KW Signal; 3D-structure.  
FT SIGNAL 1 29  
FT CHAIN 30 512  
FT ACT\_SITE 260 260  
FT ACT\_SITE 264 264  
FT ACT\_SITE 357 357  
FT METAL 133 133  
FT METAL 190 190  
FT METAL 210 210  
FT METAL 212 212  
FT METAL 223 223  
FT METAL 229 229  
FT METAL 231 231  
FT METAL 233 233  
Query Match 71.6%; Score 1947; DB 1; Length 512;  
Best Local Similarity 70.4%; Pred. No. 4.3e-124;  
Matches 340; Conservative 64; Mismatches 73; Indels 6; Gaps 3;  
QY 6 NGTMMQYFEWHLNDGNHNRRLRDASNLNRRGITAIPPAWKGTSQNDVGVGAYDLYD 65  
DB 33 NGTLMQYFEWYMPNDGQHWKRLQND SAYLAELHGTAWIPPAWKGTSQADVGVGAYDLYD 92  
QY 66 LGFBNQGTGVTYKTRTSQLESIAHAKNNGVOYGVVNNHKGGAADATENVLAVENPN 125  
DB 93 LGFHFQKGTGVTYKTKGELQSAIKSLHSRDINVGVDVINHKGGAADATEDVTAIVEDPA 152  
QY 126 NRQETSGDYTIEAWTKFDPGRGNTYSDFKWYHFDGVDWDQSRQFQNRIVYKFRGDGK 185  
DB 153 DNRNVISGEHRIKAWTHFPFGRGSTYSDFKWHYHFDGTDWDESRLK-NRIYKFO--GK 209  
QY 186 ADWEVDSNGNDYLMYADVMDHPEVNVNLRGWEWYTNLNLGDFRIDAVKHKYSF 245  
DB 210 ADWEVSNENGDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHKFSF 269  
QY 246 TRDLWTHVRNATGKEMFPAFAEFPKNDLGALENLYKTNWNSVDFVPLHYNLNASHSG 305  
DB 270 LRDNVNHVREKTKEMFTVAEYQNDLGALENLYKTNWNSVDFVPLHYQFHAASQGG 329  
QY 306 NYDMAKLLNGTGVQKHPMHAFTVFDNHDSDQPSLESFVQEWKPLAYAILIREQGPS 365  
DB 330 GYDMRKLLNSTVSKHPLKAVTFVDNHDTPQGSLESFTVQWFKPLAYAIFLTRESYPQ 389  
QY 366 VFYGDYVGIPTHS---VPAMKAKIDPILAEONFAVCTOHDYDPDHNIIGWTRGNTHP 422  
DB 390 VFYGDYVGTGDSQREIPALKHKIEPILKARKQAYGAQHDYFDHDIIVGWTREDSVA 449  
QY 423 NSGLATTMSDGPGEKWMYVQGNKQVHWDITGNKEFTVTINADGWANFSVNGSGSYIW 482  
DB 450 NSGLAALITDGPGEKWMYVGRQVQVAGETWHDITGNRSEPVVINSEGVHNGSGSYIY 509  
QY 483 VKR 485  
DB 510 VQR 512



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159 DRNQESGTTQIQAWTKDFPGRNTYSSPKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
186 AWDEWVDSNGNTDYLMYADVDMHPVAVNELRWGEWYNTNLNLCDFRIDAVKHIXYSF 245
218 AWDEWVDSNGNTDYLMYADVDMHPVAVNELRWGEWYNTNLNLCDFRIDAVKHIXYSF 277
246 TRDLWTHVRNATGKEMPAFAEFKNDLGALENYLNTKTNWHSVDPVPLHYNLNINASGG 305
278 FPDWLSVRSQTGKPLFTVGEYNSYDINKLHNYIMKTNGTMSLFDAPLHKNFYTASKSGG 337
306 NYDMAKLLNCTVVKQHPHVAFTVDNHSQGESLESFVQEWKFLAYALILRQEGYPS 365
338 TFDMTLMTLTKMOQTLAVTFVDNHDTEFGQALQSWVDPWFKFLAYALILRQEGYPC 397
366 VFYGDYIGITHSPVAMKAKIDPILKARQNFAYGTQHDYFDHNIIGWTREGNTHPNSG 425
398 VFYGDYIGITHSPVAMKAKIDPILKARQNFAYGTQHDYFDHNIIGWTREGNTHPNSG 457
426 LATIMSDGPGGKWMYVQONKAGQVWHDTGNKPGTITINADGWANFVNGSGSVIWXKR 485
458 LAALITDGPCKGKWMYVQONKAGQVWHDTGNKPGTITINADGWANFVNGSGSVIWXKR 517

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## RESULT 4

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ID AMY BACAM STANDARD; PRT; 514 AA.
AC P00692;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
OS Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH;
RX MEDLINE=83108808; PubMed=6185474;
RA Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
RA Kaeeriaeinen L.;
RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
RT deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013(1983).
RN [2]
RP SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg F.;
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
RT amylase.";
RL Biochem. J. 185:387-395(1980).
RN [3]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;
RA Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
RA Soederlund H., Takkinen K., Kaeeriaeinen L.;
RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
RT region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
RL Gene 15:43-51(1981).
RN [4]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
RT its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170(1987).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkmenburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.

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RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:19099-19107(2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; J01542; AAA22191.1; -;
DR EMBL; V00092; CAA23430.1; -;
DR EMBL; A20154; CAA01489.1; -;
DR EMBL; M18424; AAA22192.1; -;
DR PIR; A92389; ALBSN.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 514
FT ACT_SITE 262 262
FT ACT_SITE 292 292
FT ACT_SITE 359 359
FT METAL 133 133
FT METAL 190 190
FT METAL 212 212
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FT METAL 331 331
FT METAL 438 438
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FT CONFLICT 79 79
FT CONFLICT 84 84
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Best Local Similarity 67.9%; Pred. No. 5,7e-119;
Matches 330; Conservative 65; Mismatches 87; Indels 4; Gaps 2;

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QY 3 NGTGTMMQYFEWHLPNDSNHNRLRDDASLNRRGTAIWIIPAWKGTSONDVGYGAYD 62
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Dd 30 SAVNGTLUMQYFEWYTPNDGQHWKRLQNDASHLSDIGITAWIIPAYKGLSQSDNGYGYD 89
QY 63 LYDLGEFNQKGTVRTKYGTGTSQLESALHAKNNGVQYVGVVNMHKGADATENVLAVEV 122
Dd :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd 90 LYDLGEFQKGTVRTKYGTGKSELQDAIGSLHSRNVQYVGVVNLHKGADATEDVTAVEV 149
QY 123 NPNRNQIEGSDYTIETAWTKDFPGRNTYSDPKRWYHFDGVDWDSRKL-SRIYKFRG 182
Dd :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd 150 NPNRNQIEGSDYTIETAWTKDFPGRNTYSDPKRWYHFDGVDWDSRKL-SRIYKFRG 208

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QY 183 DGKAWDEVDSENGNDYLYMYADVDMDPHPVAVNELRRWGEWYNTNLNLDGFRIDAVKHK 242
Db 209 EGRKAWDEVSSENGNDYLYMYADVDMDPHPVAVNELRRWGEWYNTNLNLDGFRIDAAKHK 268
QY 243 YSTRWLTHTVRNATGKEMFAVAEPFKNDLGALENYLNTKNNHNSVDPVPLHYNLYNASN 302
Db 269 FSFLRDWQVROATGKEMFTVAEYQNNAGKLENYLNTKNNHNSVDPVPLHFNLOAAS 328
QY 303 SGGNYDMAKLNGTVVQKHPMAHTVFDNHDSPGSELESFVQWPKPLAYALILIREQG 362
Db 329 QGGYDMRLLDGTVVSRHEKAVTVFENHDTQPGSLESTVQWPKPLAYAFLIRESG 398
QY 363 YPSVFYDYGIGIPHS---VPAMKAKIDPILARQNFAYQTQHDYFDHNNIIGWTREGNT 419
Db 389 YPOVFYDGMVGTGTPKPSLKNIPIELTKARKEYAVGPQHDYIDHPDVICWTREGDS 448
QY 420 THPNSGLATIMSDPGGCKWYVQNKAGQVWDITGNKPGTITINADGWANFVNGGSV 479
Db 449 SAAKSGLAALITDPGSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGNGEHPVNDGSV 508
QY 480 SIWVKR 485
Db 509 SIYVQK 514

RESULT 5
AMV2_SALTY
ID _AMV2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR STM1963.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=SUW1103;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [3];
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=SUW1103;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [4];
RP SEQUENCE OF 476-494 FROM N.A.
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIIb, including a

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RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L01643; AAA27110.1; -.
DR EMBL; AB008787; AAL20875.1; -.
DR EMBL; M85241; AAA27079.1; -.
DR EMBL; L13280; AAA1970.1; -.
DR PIR; B45738; B45738.
DR KSSP; P06278; LVJS.
DR StyGene; SG10011; amyA.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235..235 BY SIMILARITY.
FT ACT_SITE 265..265 BY SIMILARITY.
FT ACT_SITE 332..332 BY SIMILARITY.
FT METAL 104..104 CALCIUM (BY SIMILARITY).
FT METAL 239..239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462..462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5E47C CRC64;

Query Match 39.8%; Score 1082; DB 1; Length 494;
Best Local Similarity 42.5%; Pred. No. 8.1e-66;
Matches 209; Conservative 82; Mismatches 183; Indels 18; Gaps 6;

QY 6 NGTMQYFEWHLFNDGNHNRRLRDDASLRNRGITAIIWIPPAWKGTSON-DVGYGAYDLY 64
Db 3 NPTLLQYFHWYVDPGGLWSELAERADGLNDGINWVLPFPACKGASGGVSGYDYDLF 62
QY 65 DLGEFNQKGTVTIKYGRSQAESAHLKXNGVQVYGVDMVHMKGCADATENVLAVENP 124
Db 63 DLGEFDQKGTIATKYGRQLLTALDALKKNIAVLDDVNVHMGADDEKERIRVORVQ 122
QY 125 NNRNQEISGDYTIAMTKDFPGRGNTYSDFKRWYHFDGVDWDQSRQFNRIYKFRGD- 183
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QY 184 -GKAMDWEYDSENGNDYLYMYADVDMDPHPVAVNELRRWGEWYNTNLNLDGFRIDAVKHK 242
Db 182 TGDGWNQDQVDEMGNFDYLMGENIDPRNHAHTVEIKYWARVWVMEQTHCDGFRIDAVKHIP 241
QY 243 YSFTRDLWLTHTVRNATGKEMFAVAEPFKNDLGALENYLNTKNNHNSVDPVPLHYNLYNASN 302
Db 242 AMFYKEWIEHVVQAVAPKPLFIVAEYVSHVSDKLTQYIDQVQDKTMLFDAPLQMKFHEASR 301
QY 303 SGGNYDMAKLNGTVVQKHPMAHTVFDNHDSPGSELESFVQWPKPLAYALILIREQG 362
Db 302 QGAEDVMRHI FTGTLVEADPFHATVLVANDTQPLQALEAPVEPWFKPLAYALILIRENG 361
QY 363 YPSVFYDYGIGIPHS-----SVPAMKAKIDPILARQNFAYQTQHDYFDHNNI 411
Db 362 VPSVFYDLYGASYESGSENGETCTCRVDMFVIN-QLDRLILARQRFAGHGTTLFFDHPNCI 420
QY 412 GWTREGNTTHPNSGLATIMSDPGGCKWYVQNKAGQVWDITGNKPGTITINADGWAN 471

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Db 421 AFRSG--TEENPCVVVLNGDDGKTKLLGDNANYANKWRDFLGNRDEYVVTNDQGEAT 478
QY 472 FSVNGGVSIVW 483
Db 479 FFCNAGSVSVW 490

RESULT 6
ID AMY2_ECOLI
AC P26612; P78072; STANDARD; PRT; 495 AA.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylose (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAIL;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylose, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251359; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=JAIL;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065 (1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=JAIL;
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIb, including a
RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; L01642; AAA23810.1; -.
CC EMBL; AB000285; AAC74994.1; -.
CC EMBL; D90833; BAA15755.1; -.
CC EMBL; M85240; -; NOT ANNOTATED_CDS.
CC EMBL; L13279; AAA82575.1; -.
CC PIR; D64956; A45738.
CC HSP; P06278; 1VJS.
CC EcoGene; EG11387; amyA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC Pfam; PF00128; alpha-amylose; 1.
CC SMART; SM00642; Aamy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 19 20 KL -> SS (IN REF. 1).
FT CONFLICT 109 109 A -> V (IN REF. 1).
FT CONFLICT 149 149 Q -> E (IN REF. 1).
FT CONFLICT 234 234 L -> I (IN REF. 1).
FT SEQUENCE 495 AA; 56639 MW; 26AFF6797DDA54D6 CRC64;
SQ
Query Match 39.1%; Score 1064; DB 1; Length 495;
Best Local Similarity 41.9%; Pred. No. 1.3e-64;
Matches 206; Conservative 86; Mismatches 182; Indels 18; Gaps 6;
QY 6 NGTMQYFEWHLNDGNHNLRLDDASNLNRGITAIPPAKGTQSN-DVUGYGYDLY 64
DB 3 NPTLLQCFHWYPEGGKLPDLAERADGFNDIGINVMPLPYPAYKGGSGVSGVSYDLF 62
QY 65 DLGEFNQKGTVRTKYGTRSOLESAIHALKONGVQVYGVDMNHKGGADANVLAVEVNP 124
DB 63 DLGEFDQKGSIPKYGDQAQLAALDALKRNDIAVLDDVVVNHKMGADKEAIRVQRVNA 122
QY 125 NNRNQISGDYTTIEAWTKFDPPGRGNTYSDPKRWYHFDGVDWDQSRQFQNRYYKFRGD- 183
DB 123 DDRQTDEETIECEGWTRYTFPARAGQYSQFIWDFKFCFGIDHNPD-EDGIFKIVNDY 181
QY 184 -GXANDWEVDSENGVDYLMYADVMDHDPVNVNELRRWGEWYNTNLNDFRIDAIVKHK 242
DB 182 TGEWMDQVDDDELGNFDYLMGENIDFRNHAIVTEIKYWARVWVMEQTQCDGFRDLAVKHIP 241
QY 243 YSTFDWLTHVRNATKEMFAVAEFKWNLDGALENLYLNKTNHNSVDFDPLHLYNLNASN 302
DB 242 ANFYKEMIEHVQEVAPKPLFVIAEYWSHEVDKLTQTYIDQVEGKTMFLDAPLQMKFHEASR 301
QY 303 SGGNYDMAKLLNGTVVQKHPMHAVTVDNHDSDQGESLESFVQSWFKPLAYALILTREOG 362
DB 302 MGRDYDMTQITFTGLVEADFFHVLTVANHDTQLQALEAPVPEVPKFLAYALILLRENG 361
QY 363 YPSVYFGDYGIPTHSV-----PAMKAKIDPILAEARONFAYGTQHDYFDHNNII 411
DB 362 VPSVYFDLYGAHYEDVGGDGQTYPTIDMPIIE-QLDELILARQRFAGHVQTLFFDHPNCI 420
QY 412 GWTREGNTHPNGLATINSDGPGKWMYVGONKAGQVWHHDITGNKPGVTTNADGWAN 471
DB 421 AFRSGTDEFP--GCVVMMSGDDGDKTIHLGNYGNKTRWDRFLGNRQERKQVTDNGEAT 478

```

QY 472 FSVNGGVSIVWY 483  
 Db 479 FFCNGGVSIVWV 490

RESULT 7  
 AMYB\_PABPO STANDARD; PRT; 1196 AA.  
 AC P21543;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Beta/alpha-amylase precursor [includes: Beta-amylase (EC 3.2.1.2);  
 DE Alpha-amylase (EC 3.2.1.1)]  
 OS Paenibacillus polymyxa (Bacillus polymyxa).  
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.  
 OC NCBI\_TaxID=1406;  
 RN [1]  
 RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=72;  
 RX MEDLINE=87165765; PubMed=2435707;  
 RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,  
 RA Tsukagoshi N., Uda S.;  
 RT "Cloning and nucleotide sequence of the gene coding for enzymatically  
 RT active fragments of the Bacillus polymyxa beta-amylase.";  
 RL J. Bacteriol. 169:1564-1570(1987).  
 RN [2]  
 RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=72;  
 RX MEDLINE=89123046; PubMed=2464578;  
 RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,  
 RA Tsukagoshi N., Uda S.;  
 RT "A single gene directs synthesis of a precursor protein with beta-  
 RT and alpha-amylase activities in Bacillus polymyxa.";  
 RL J. Bacteriol. 171:375-382(1989).  
 RN [3]  
 RP SEQUENCE OF 1-776 FROM N.A.  
 RC STRAIN=ATCC 8523;  
 RX MEDLINE=87231094; PubMed=2438660;  
 RA Rhodes C., Strasser J., Friedberg F.;  
 RT "Sequence of an active fragment of B. polymyxa beta amylase.";  
 RL Nucleic Acids Res. 15:3934-3934(1987).  
 RN [4]  
 RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.  
 RX MEDLINE=91215008; PubMed=1827035;  
 RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;  
 RT "Structural and functional roles of cysteine residues of Bacillus  
 RT polymyxa beta-amylase.";  
 RL Biochemistry 30:4594-4599(1991).  
 CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO  
 CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER  
 CC SECRETION.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in  
 CC polysaccharides so as to remove successive maltose units from the  
 CC non-reducing ends of the chains.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
 CC linkages in oligosaccharides and polysaccharides.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of  
 CC glycosyl hydrolases.  
 CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of  
 CC glycosyl hydrolases.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M15817; AAA85446.1; -;  
 CC EMBL; Y00150; CAA68344.1; -;

DR PIR; A29130; A29130.  
 DR HSSP; P36924; 1B9Z.  
 DR InterPro; IPR006589; Alp\_amyl\_cat sub.  
 DR InterPro; IPR006048; Alpha\_amyl\_C.  
 DR InterPro; IPR006047; Alpha\_amyl\_cat.  
 DR InterPro; IPR005085; CBM\_25.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR InterPro; IPR001554; Glyco\_hydro\_14.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR Pfam; PF02806; alpha-amylase\_C; 1.  
 DR Pfam; PF03423; CBM\_25; 2.  
 DR Pfam; PF01373; Glyco\_hydro\_14; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR PRINTS; PR00750; BETAAMYLASE.  
 DR SMART; SM00642; Amy; 1.  
 DR SMART; SM00632; Amy\_C; 1.  
 DR PROSITE; PS00506; BETA-AMYLASE 1; 1.  
 DR PROSITE; PS00679; BETA-AMYLASE 2; 1.  
 DR KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;  
 KW Polysaccharide degradation; Repeat.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.  
 FT DOMAIN 36 454 BETA-AMYLASE.  
 FT REPEAT 455 558  
 FT REPEAT 565 668  
 FT DOMAIN 669 1196 ALPHA-AMYLASE.  
 FT DISULFID 118 126  
 FT ACT\_SITE 198 198  
 FT ACT\_SITE 394 394  
 FT MUTAGEN 118 118  
 FT MUTAGEN 126 126  
 FT MUTAGEN 358 358  
 FT CONFLICT 1 1  
 FT CONFLICT 67 67  
 FT CONFLICT 100 100  
 FT CONFLICT 154 154  
 FT CONFLICT 177 177  
 FT CONFLICT 227 228  
 FT CONFLICT 330 330  
 FT CONFLICT 425 425  
 FT CONFLICT 493 493  
 FT CONFLICT 532 532  
 FT CONFLICT 559 559  
 FT CONFLICT 665 665  
 FT CONFLICT 681 681  
 FT CONFLICT 686 686  
 FT CONFLICT 725 728  
 FT CONFLICT 736 736  
 FT CONFLICT 741 741  
 FT CONFLICT 758 758  
 SQ SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;

Query Match 12.0%; Score 327; DB 1; Length 1196;  
 Best Local Similarity 23.4%; Pred. No. 1.8e-14;  
 Matches 121; Conservative 70; Mismatches 192; Indels 134; Gaps 24;

QY 1 HNGTNGTMMQVFEWHLPLNDGNHNLRLDDASNLNLRGRTAIWIPPAWKGTSQNDV-GYG 59  
 Db 766 NYGFFNSNNSDQKWH-----GGDFGIIKLDYIKNMGFTAIWITPTVMQKSEYAYHG 821  
 QY 60 AYDLVDLGEFNQKGFVTRKYKTRSOLESAIHALKNGVGVYGDVVMNHKGGADATENVLA 119  
 Db 822 TYDFY-----AVDGLGTMDKQLKELVRAKHAIDKNAVMVDVVVNHG----- 862  
 QY 120 VEVNPNNEQISGDYITTEATWKDF-PCRNTYSDR-KWEYHFDGVDWQDSQFQNR 177  
 Db 863 -----DFQNGFAPKAPFDKADWYHHNGITITGDVYNNNQ- 897  
 QY 178 YKFRGDGKAWDEVDSENGNDYLMADVMDHPEVNVNELRRWGEWYTNNTLMDGFRIDA 237  
 Db 898 -----WKL--ENG--DVAGLDLDNHNENPATANELKNKWLNETGIDGLRDT 942  
 QY 238 VKHIKYSFTRDLWLTNRNATCKEMFAVAFWKNLDGALENLYNKTNNWNSHSDVDFPLHNL 297







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FT STRAND 383 387
FT STRAND 393 398
FT STRAND 403 408
FT HELIX 415 417
FT TURN 418 418
FT STRAND 424 429
FT TURN 430 433
FT STRAND 434 438
SQ SEQUENCE 548 AA; 59876 MW; 2B87217B3379158F CRC64;

Query Match 10.1%; Score 275; DB 1; Length 548;
Best Local Similarity 25.5%; Pred. No. 2.3e-11;
Matches 133; Conservative 64; Mismatches 167; Indels 158; Gaps 28;

QY 2 HNGTNGTMMQYFEHL-----PNDGNHNRRLRDDASNLNRGITAITWPPAWKGTSONDVG 57
DB 33 YHGDEIILQGFHNWVREAPND--WYNILRQQAATTAADGFSALWVPWRDSSWSGD 90
QY 58 --YGAYDLYDLGEPNKGVTYKGTROLESALHAKNGVQVGVVNMH--KGADA 113
DB 91 SKSGGEGYFHWDFNKG---RYGSDAQLRQAASALGGAGVKLYDVVPHNMNRGYPDK 146
QY 114 TENVLAVEVPPNENQISGDYITTEATKEDFPGRGNTYSDFKRWYHFDGVDWDQSRQF 173
DB 147 EINLPAG-----QGFWRNDADPGN-YFN-----DCDDGDRF 177
QY 174 QNRIYKFRGKAWDEVDSENGNYDLYMTADVMDHPPEVNNELRRGWGWTN---TLNL 230
DB 178 -----IGGD-----ADLNTGHPVYGMER---DEFTNLRSQYGA 208
QY 231 DGRFRIDAVKHIXFTDRDLWTHVRNATGEMFAVAEPWKNLDLGALE-----NYLNKTNWNH 286
DB 209 GGRFRDFVRGYPVPRVNSWMTD---SADNSFCVGLWK---GPSEYPNMDWRNTASWQ 261
QY 287 -----SVEFVPLHNLNYSNSGNYDMAKLLNGTVQKHPHMAVTFVDNHD- 334
DB 262 IIKWSDRAKCPVDFDFALKERMONGSIA---DWKHGLNGNPDPRWRREAVTFVDNHDG 317
QY 335 -----QPCELESFVQEFKPLAYALITLTREQYPSVF-----YGDYTGIPHSVPAM 382
DB 318 YSPQNGQGHWAQDGLIRQAYAILT-SPGTPVYVWSHMYDWGYGDF----- 365
QY 383 KAKIDPILAEQONPAYQTQHDYFDHNIIGWTRGNTTHPNSGIATIMSDPGGKRWYV 442
DB 366 ---IRQLIQVR--AAGVRAD-----SAISFHSYSGLVATVSGSQQLLV 406
QY 443 QNKAGQVWHDITGKGTGVTINADGNANFSVN--GGSVSIW 482
DB 407 ALNS-----DL-GN-PCQV---ASGSFSEAVNASGQVRVW 437

RESULT 10
AM3A_ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE Glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).

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CC -!- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
CC -!- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56336; CAA39776.1; -.
CC PIR; S14958; S14958.
CC HSP; P04063; IAVA.
CC Gramene; P27932; -.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC Signal; Multigene family.
CC FT SIGNAL 1 26
CC FT CHAIN 27 440
CC FT ACT_SITE 207 207
CC FT ACT_SITE 315 315
CC FT METAL 119 119
CC FT METAL 145 145
CC FT METAL 155 155
CC FT METAL 166 166
CC FT METAL 169 169
CC FT METAL 170 170
CC FT METAL 171 171
CC FT METAL 174 174
CC FT METAL 176 176
CC FT METAL 177 177
CC SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 10.1%; Score 274.5; DB 1; Length 440;
Best Local Similarity 24.4%; Pred. No. 1.9e-11;
Matches 112; Conservative 55; Mismatches 167; Indels 125; Gaps 19;

QY 9 MMQYFEW-HLPNDGNHNRRLRDDASNLNRGITAITWPPAWKGTSONDVGAYDLVGL 67
DB 31 LFQGFNWDSSKQGGWYMLKQVGDIASAGVTHVLPPTTHSVSPQ--GYMPGLYDLN 88
QY 68 EFNKGTVTRKYTRSOLESALHAKNGVQVGVVNMHKGADATENVLAVEVNNR 127
DB 89 -----ASKYGTGKAEKSLIAAFHAKGKCVADIVNHRCAD- 125
QY 128 NOEISGDYITEATKEDFPGRGNTYSDFKRWYHFDGVDWDQSRQFONRYKFRGDGKAW 187
DB 126 -KQGRGVYCI-----FKGGPR-----GCLDWGPSMCCDDTQYSDGTG--- 163
QY 188 DWEVDSENGNYDLYMTADVMDHPPEVNNELRRGWGWTNLTNLDFRIDAVKHIXYFTR 247
DB 164 -----HRTGADFAAAPDIDHNLPLVQRELSDWLRRLRVDVFGDWRLDFAKGYSAVAR 218
QY 248 DMLTHVRNATGEMFAVAEPWKNLDG-----ALENYLNKTNWNHVSFV 291
DB 219 ---TYVQNA--RPSFVVAEIV--NSLSYDGDGKPAANQDQGRQELVNVVVKVGGSPATADF 272

```

QY 292 PLHYNLNYSNNGYDWMKLLNGT---VVQKHPHVAITFVDNHDSPGSLSEFVQEWFP 348  
 Db 273 TTGKILSAVQ---GELWRMRDKGKAPGMIGWYKAVTFVDNHDGTGSTRM-----WP 324  
 QY 349 KP-----LAYALITREQYPSVFGYDYGIPHTSVPMKAKIDPILKARQNPAYGTOHD 403  
 Db 325 FPSDKVILGYAYILT-HPGVPCIFYD-----QVFDWNLKQE 359  
 QY 404 YFDHNNIGWTRGNTHTPNSGLATIMSDGPGGKWMYV 442  
 Db 360 I---NALAATKRGINAGSKLRVL-----AAESDMYV 389

RESULT 11  
 ID AM3D ORYSA STANDARD; PRT; 435 AA.  
 AC P27933;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan  
 DE glucanohydrolase).  
 GN AMY1.3 OR AMY3D.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;  
 RX MEDLINE=9108278; PubMed=2263460;  
 RA Huang N., Koizumi N., Reinl S., Rodriguez R.L.;  
 RA "Structural organization and differential expression of rice alpha-  
 RT amylase genes";  
 RL Nucleic Acids Res. 18:7007-7014(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A. (CLONE POS137).  
 RX MEDLINE=90318322; PubMed=2370848;  
 RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,  
 RA Rodriguez R.L.;  
 RT "The alpha-amylase genes in Oryza sativa: Characterization of cDNA  
 RT clones and mRNA expression during seed germination";  
 RL Mol. Gen. Genet. 221:235-244(1990).  
 CC -1- FUNCTION: Important for breakdown of endosperm starch during  
 CC germination.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
 CC linkages in oligosaccharides and polysaccharides.  
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).  
 CC -1- SUBUNIT: Monomer.  
 CC -1- TISSUE SPECIFICITY: Is expressed in all tissues, except in  
 CC immature seeds. Is the most abundant alpha-amylase isozyme in  
 CC callus.  
 CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination  
 CC in the aleurones cells under the control of the plant hormone  
 CC gibberellic acid and in the developing grains at a low level.  
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
 CC  
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 CC  
 CC EMBL; M59351; AAA33895.1; -;  
 CC EMBL; M24287; AAA33886.1; -;  
 CC PIR; S12625; S12625.  
 CC HSSP; P04063; IAVA.  
 CC Gramene; P27933; -;  
 CC InterPro; IPR006589; Alp\_amy1\_cat\_sub.

DR InterPro; IPR006047; Alpha\_amy1\_cat.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR SMART; PR00110; ALPHAAMYLASE.  
 DR SMART; SM00642; Amy; 1.  
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
 KW Signal; Multigene family.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 435 ALPHA-AMYLASE ISOZYME 3D.  
 FT ACT\_SITE 203 203 BY SIMILARITY.  
 FT ACT\_SITE 311 311 BY SIMILARITY.  
 FT METAL 116 116 CALCIUM 1 (BY SIMILARITY).  
 FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 136 136 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 138 138 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 141 141 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 151 151 CALCIUM 3 (BY SIMILARITY).  
 FT METAL 162 162 CALCIUM 3 (BY SIMILARITY).  
 FT METAL 167 167 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY  
 FT METAL 170 170 SIMILARITY).  
 FT METAL 172 172 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY  
 FT METAL 173 173 SIMILARITY).  
 FT CONFLICT 73 74 CALCIUM 1 AND 3 (BY SIMILARITY).  
 FT CONFLICT 137 137 PQ -> R (IN REF. 2).  
 FT CONFLICT 137 137 P -> R (IN REF. 2).  
 SQ SEQUENCE 435 AA; 47911 MW; 1BBD6AB195BA0D6E CRC64;  
 Query Match 9.7%; Score 264.5; DB 1; Length 435;  
 Best Local Similarity 22.5%; Pred. No. 8.8e-11;  
 Matches 120; Conservative 63; Mismatches 171; Indels 179; Gaps 26;  
 QY 2 HNGTNGTMMQYFEWH-LPNDGNHNRRLRDDASNLNRGTAIWIPPAWKGTSQNDVGYGA 60  
 Db 21 NSQQAQLFQGFNWSKQGGWYNMLKGQVDDIAKAGVTHVWLPSPSHVAPQ--GYMP 78  
 QY 61 YDLYDLGEFNQGTVRTKYGTSQLESATHALKNNGVQVGVGVMMHKGADATENVLAV 120  
 Db 79 GRLYDLDD-----ASKYGTAAELKSLTAAPFHGKGVQCVADVIVNHRCA----- 120  
 QY 121 EVNPNRNQIEISGDYVTEAWTKFPFGRGNTYSDPKRWYHFDGVDW-----DOSRQF 173  
 Db 121 -----EKDARGVVCV-----FE-----GGTP-----DRLDWGPGMCSDDTQVS 155  
 QY 174 QNRIYKFRGDKAWDEVDSENGYDYLMYADVMDH--PEVYNELRRWGEWYTNLTNLD 231  
 Db 156 DGTGHRDTGEG-----FGAAPDIDHLNPRVQRELTDLNMLKSDVGFD 198  
 QY 232 GERIDAVKHKYSFTEDMLTHVRN---ATGKEMFAVAEPKN-----DLGAL 275  
 Db 199 GWRLLD-----FAKGYSTDIAKMYVESCKPGFVVVAEINWSLSYNGDGKPAANOQGRQ 250  
 QY 276 E--NYLNTKNWNSVDFDVLPHNLNYSNNGYDWMKLLNGT-----VVQKHPHVAITF 328  
 Db 251 ELVNVNVAVGGAFTFD-----FTTKGLQAGVQGELWRLRDNGKAPGMIGWLPKAVTF 306  
 QY 329 VDNHDSQPGESLESFVQEWKPL-AYALITREQYPSVFGYDYGIPHTSVPMKAKID 387  
 Db 307 VDNHDTGTSQKLWPPPSD--KVMQGVAYILT-HPGVPCIFY----- 344  
 QY 388 PILEARQNPAYGTOHDYFDHNNIGWT-----REGNTHTPNSGLATIMSDPG- 435  
 Db 345 -----DH--MFDWNLKQETALAAIRERNGINAGSKLRIVWADADAY 384  
 QY 436 ----GEKWMYVQNKAGQGVWHDITGNKPGTIVTINADGWANFSVNGSVSIWVK 484  
 Db 385 VAVVDEKVMV----KIG-TRYDVGNVPSDF-----HQTVHGKDISVWEK 424

RESULT 12  
 AMT4\_PSESA  
 ID AMT4\_PSESA STANDARD; PRT; 551 AA.  
 AC P22963;  
 DT 01-AUG-1991 (Rel. 19, Created)





Db 27 LFOGFNWSKXNGWTFNLMGKYDDIAAGITHVWLPASQSAEQ--GYMGRLYDLD 84  
 Qy 68 EFNQKGTVRTYKTRQSAIAHALKXNGVQVGVVNMHKGADATENVLAEVNPNNR 127  
 Db 85 -----ASKYGNKAQLKSLGALHGKGVKAIAIVINHR-----TAE 120  
 Qy 128 NOEISGDYTIENATKTFDFPGRGNTYSDPKRWYHFDG-----VDWQSRQFQNRYYKFR 181  
 Db 121 HKDGRGIYCI-----FEGGTPDARLDWGP-----HMC 148  
 Qy 182 GDGKAWDEVDSENGNDYLMYADVMDHDPVNNELRWGEWYTNLNLGDFRIDAVKHI 241  
 Db 149 RDRPYADGTGNTGADFGAIPDIDLNLVQKELVNLWADKIDGFGWRFDPAKY 208  
 Qy 242 KYSTRDMLTHVRNATKEMPAFAEFW-----KNDLGALENYLKNWNHSHV----- 288  
 Db 209 SADVAKIYIDR-----SEPSFAVAEITWTSLAYGDKGPNLQDQHRQELVNWVDKVGKG 263  
 Qy 289 -----FDVPLHYNLYNASNGNYDMAKLLNGT-----VVOXHPMHAVTFVDNHDSPGE 338  
 Db 264 PATTFDFTTK--GILNVAVEGLW-----RLRGTGKAFCMIGWPAKAVTFVDNHDGTSQ 318  
 Qy 339 SLESFVCEWFKPLAYALILTRQGVPSVFYGYGIPTHSVPAKAKIDPILAEARQNFAY 398  
 Db 319 HMPFPFSDRWQ--GYAILT--HPTGTCIFYDHFDM-----GLKBEIDLVSUR----- 365  
 Qy 399 GTQHDYDFDHNIIIGWTRGNTHPNGLATIMSPGCGEKWYVQNKAGQV-----WH 452  
 Db 366 -----TRHG--IHNEKLIQIEADAD-----LYLAEID--GRKIVKLGPY 402  
 Qy 453 DITGNKGTGVTINADGNVSNVSGSVSIWK 484  
 Db 403 DVGNLIPGFKVAA-----HGNDYAVWEK 426

## RESULT 14

CDGT\_BACS8  
 ID CDGT\_BACS8 STANDARD; PRT; 713 AA.  
 AC P17692;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Cyclomaltoextrin glucanotransferase precursor (EC 2.4.1.19)  
 DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting  
 DE amylase).  
 OS Bacillus sp. (strain B1018).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1417;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.  
 RX MEDLINE=90147765; PubMed=1689153;  
 RA Itokor P., Tsukagoshi N., Uda S.;  
 RT "Nucleotide sequence of the raw-starch-digesting amylase gene from  
 RT Bacillus sp. B1018 and its strong homology to the cyclodextrin  
 RT glucanotransferase genes."  
 RL Biochem. Biophys. Res. Commun. 166:630-636(1990).  
 CC -!- FUNCTION: This endo-type adsorbable amylase is capable to  
 CC digest raw starch.  
 CC -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation  
 CC of a 1,4-alpha-D-galactosidic bond.  
 CC -!- COFACTOR: Binds 2 calcium ions per subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See [http://www.iesb-sib.ch/](http://www.iesb-sib.ch/announce/)  
 CC or send an email to [license@iesb-sib.ch](mailto:license@iesb-sib.ch)).  
 CC -----  
 CC EMBL; M33302; AAA22239.1; -.

DR EMBL; D90112; BAA14140.1; -.  
 DR PIR; S09196; S09196.  
 DR HSP; P43379; ICDG.  
 DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
 DR InterPro; IPR006048; Alpha\_amy1\_C.  
 DR InterPro; IPR006047; Alpha\_amy1\_cat.  
 DR InterPro; IPR002044; CBD\_4\_amy1\_cat.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR002909; IPT\_TIG.  
 DR Pfam; PF001128; alpha-amy1ase; 1.  
 DR Pfam; PF02806; alpha-amy1ase\_C; 1.  
 DR Pfam; PF00686; CBM\_20; 1.  
 DR Pfam; PF01833; TIG; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR ProDom; PD001568; CBD\_4; 1.  
 DR SMART; SM00642; Amy; 1.  
 DR SMART; SM00632; Amy\_C; 1.  
 KW Transferase; Glycosyltransferase; Calcium-binding; Signal.  
 FT SIGNAL 1 27  
 FT CHAIN 28 713  
 FT ACT\_SITE 256 256  
 FT ACT\_SITE 284 284  
 FT ACT\_SITE 355 355  
 FT METAL 54 54  
 FT METAL 56 56  
 FT METAL 59 59  
 FT METAL 60 60  
 FT METAL 80 80  
 FT METAL 166 166  
 FT METAL 217 217  
 FT METAL 226 226  
 FT METAL 260 260  
 FT METAL 260 260  
 SQ SEQUENCE 713 AA; 77420 MW; 85FB616DA687B888 CRC64;  
 Query Match 9.6%; Score 262; DB 1; Length 713;  
 Best Local Similarity 21.6%; Pred. No. 2.3e-10;  
 Matches 112; Conservative 88; Mismatches 183; Indels 136; Gaps 24;  
 Qy 21 GNHW-----NRLRDDASNLNRGTAIWIPPAWK-----TSQNDVGYGAYDLYDGEF 69  
 Db 78 GGDWQGIINKIND--GYLTGMGVTAIWISQFVENIYSIYSGVNNYTHGYWARDPKKT 135  
 Qy 70 NQKGTVRTYKTRQSAIAHALKXNGVQVGVVNMHKGADATENVLAEVNPNNR-- 127  
 Db 136 N-----PAYGTTADFQNLIAAHAKNKIIVIDPAPNHTSPASSDQSPFA-----ENGLY 185  
 Qy 128 -NOEISGDYTIENATKTFDFPGRGNTYSDPKRWYHFDGVDWQSRQFQNRYYKFRGDGA 186  
 Db 186 DNGTLLGGYT-----NDTNLPHHNGTDFS----- 211  
 Qy 187 WDWEVDSENGNDYLMYADVMDHDPVNE-----LRRGEWYTNLNLGDFRIDAVKH 240  
 Db 212 -----TTENGIIYKNL--YDLADLNHNSTSDVYLKDAIKMMLD-----LGIDGIRMDAVKH 260  
 Qy 241 IKYSFTDMLTHVRNATKEMPAFAEFW--KNDLGALENYLKNWNHSHVDFVPLHYNLY 298  
 Db 261 MPFGWQKSFMAAVNNY--KPVFTFGWFLGVNEVGP--ENHKFANESGMSLLDFFPAQKVR 317  
 Qy 299 NA--SNSGNYVDMAKLLNGTVQKHPM--HAVTFVDNHDSPGSELESFVQWFKPLAYAL 355  
 Db 318 QVPEDNTDNYGLKAMLEGSADYAQVDDQVTFIDNHDMERFHASNARRKLEQALAFLL 377  
 Qy 356 ILTRQGVPSVFYG--DYV-----GIPTHSVPA-----MKAKIDPILAEARQNFAY 399  
 Db 378 ILAR---VPAIYYTEQYMSGGTDPDNRARIPSPSTSTTAYQVQIKLAPLRKSNPAIAYG 434  
 Qy 400 TQHDYDFDHNIIIGWTRG-----NTTHPNSGLATIMSDGPGGEGKWKYVQNK 446  
 Db 435 STQERWINNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSDFQGS----- 482







Db 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
QY 61 YDLIDLGEFNQKGTVRTKYGTSQLESALHALKNNGVQYGVVNMHKGADATENVLAV 120  
Db 61 YDLIDLGEFNQKGTVRTKYGTSQLESALHALKNNGVQYGVVNMHKGADATENVLAV 120  
QY 121 EVNPNRNQEIISGDYTIETAWTKFDPGRGNTYSDFKRWYHFDGVDMQDQSRQFNRIYKF 180  
Db 121 EVNPNRNQEIISGDYTIETAWTKFDPGRGNTYSDFKRWYHFDGVDMQDQSRQFNRIYKF 180  
QY 181 RGDGKAWDEVDSENGNTDYLMDVMDHPVNMELRWGEWYTNLTNLGDFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNTDYLMDVMDHPVNMELRWGEWYTNLTNLGDFRIDAVKH 240  
QY 241 IKYSFTRDLWTHVRNATGKEMFAVAFWKNDLGALENYLNKTNMNSVDFVPLHYNLYNA 300  
Db 241 IKYSFTRDLWTHVRNATGKEMFAVAFWKNDLGALENYLNKTNMNSVDFVPLHYNLYNA 300  
QY 301 SNSGGNYDMAKLLNGTVVQKHPMHAIVTVDNHDSQGESLESFVQEWFKPLAYALILTRE 360  
Db 301 SNSGGNYDMAKLLNGTVVQKHPMHAIVTVDNHDSQGESLESFVQEWFKPLAYALILTRE 360  
QY 361 QGYPVSFVGYDYGIPTHSVPAMKAKIDPILBARONFAVGTQHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPVSFVGYDYGIPTHSVPAMKAKIDPILBARONFAVGTQHDYFDHNNIIGWTREGNTT 420  
QY 421 HPNSGLATIMSDGPGGKMWYVGQKAGQVWHDTGNKPGTGTINADGWANFVSNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKMWYVGQKAGQVWHDTGNKPGTGTINADGWANFVSNGGSVS 480  
QY 481 IWVKR 485  
Db 481 IWVKR 485

## RESULT 2

US-08-861-837-2  
; Sequence 2, Application US/08861837  
; Patent No. 5856164  
; GENERAL INFORMATION:  
; APPLICANT: Ottrup, Helle  
; APPLICANT: Bisgaard-Frantzen, Henrik  
; APPLICANT: Ostergaard, Peter Rahbek  
; APPLICANT: Rasmussen, Michael Dolberg  
; APPLICANT: Van Der Zee, Pia  
; TITLE OF INVENTION: Alkaline Bacillus Amylase  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: No. 58561640 No. 5856164disk of No. 5856164th America  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,837  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,803  
; FILING DATE: 01-June-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harrington, James J.  
; REGISTRATION NUMBER: 38,711  
; REFERENCE/DOCKET NUMBER: 4157.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 867-0123  
; TELEFAX: (212) 878-9655

## ; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-861-837-2

Query Match 100.0%; Score 2720; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 2.4e-232;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Db 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
QY 61 YDLIDLGEFNQKGTVRTKYGTSQLESALHALKNNGVQYGVVNMHKGADATENVLAV 120  
Db 61 YDLIDLGEFNQKGTVRTKYGTSQLESALHALKNNGVQYGVVNMHKGADATENVLAV 120  
QY 121 EVNPNRNQEIISGDYTIETAWTKFDPGRGNTYSDFKRWYHFDGVDMQDQSRQFNRIYKF 180  
Db 121 EVNPNRNQEIISGDYTIETAWTKFDPGRGNTYSDFKRWYHFDGVDMQDQSRQFNRIYKF 180  
QY 181 RGDGKAWDEVDSENGNTDYLMDVMDHPVNMELRWGEWYTNLTNLGDFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNTDYLMDVMDHPVNMELRWGEWYTNLTNLGDFRIDAVKH 240  
QY 241 IKYSFTRDLWTHVRNATGKEMFAVAFWKNDLGALENYLNKTNMNSVDFVPLHYNLYNA 300  
Db 241 IKYSFTRDLWTHVRNATGKEMFAVAFWKNDLGALENYLNKTNMNSVDFVPLHYNLYNA 300  
QY 301 SNSGGNYDMAKLLNGTVVQKHPMHAIVTVDNHDSQGESLESFVQEWFKPLAYALILTRE 360  
Db 301 SNSGGNYDMAKLLNGTVVQKHPMHAIVTVDNHDSQGESLESFVQEWFKPLAYALILTRE 360  
QY 361 QGYPVSFVGYDYGIPTHSVPAMKAKIDPILBARONFAVGTQHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPVSFVGYDYGIPTHSVPAMKAKIDPILBARONFAVGTQHDYFDHNNIIGWTREGNTT 420  
QY 421 HPNSGLATIMSDGPGGKMWYVGQKAGQVWHDTGNKPGTGTINADGWANFVSNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKMWYVGQKAGQVWHDTGNKPGTGTINADGWANFVSNGGSVS 480  
QY 481 IWVKR 485  
Db 481 IWVKR 485

## RESULT 3

US-08-600-656-2  
; Sequence 2, Application US/08600656  
; Patent No. 6093562  
; GENERAL INFORMATION:  
; APPLICANT: Bisgaard-Frantzen, Henrik  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Borchert, Torben Vedel  
; TITLE OF INVENTION: AMYLASE VARIANTS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.  
; STREET: 405 Lexington Avenue, Suite 6400  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:



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; ORGANISM: Bacillus sp.
US-09-170-670-8

Query Match
 100.0%; Score 2720; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 H H N G T G T M M Q Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60
Db 1 H H N G T G T M M Q Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60

QY 61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V M M H K G G A D A T E N V L A V 120
Db 61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V M M H K G G A D A T E N V L A V 120

QY 121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180
Db 121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180

QY 181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N D G F R I D A V K H 240
Db 181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N D G F R I D A V K H 240

QY 241 I K Y S F T R D W L T H V R N A T G K E M F A V A E F W K N D L G A L E N Y L N K T N W N H S V F D V P L H Y N L Y N A 300
Db 241 I K Y S F T R D W L T H V R N A T G K E M F A V A E F W K N D L G A L E N Y L N K T N W N H S V F D V P L H Y N L Y N A 300

QY 301 S N S G G N Y D M A K L I N G T V V Q K H P M H A V T F V D N H D S Q P G E S L E S F V Q S W F K P L A Y A L I L T R E 360
Db 301 S N S G G N Y D M A K L I N G T V V Q K H P M H A V T F V D N H D S Q P G E S L E S F V Q S W F K P L A Y A L I L T R E 360

QY 361 Q G Y P S V F Y G D Y G I P T H S V P A M K A K I D P I L E A R Q N F A Y G T Q H D Y F D H N I I G W T R E G N T T 420
Db 361 Q G Y P S V F Y G D Y G I P T H S V P A M K A K I D P I L E A R Q N F A Y G T Q H D Y F D H N I I G W T R E G N T T 420

QY 421 H P N S G L A T I M S D G P G G E K M Y V Q N K A G Q V W H D I T G N K P G T V T I N A D G W A N F S V N G G S V S 480
Db 421 H P N S G L A T I M S D G P G G E K M Y V Q N K A G Q V W H D I T G N K P G T V T I N A D G W A N F S V N G G S V S 480

QY 481 I W V K R 485
Db 481 I W V K R 485

RESULT 6
US-09-193-068-2
; Sequence 2; Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjøluff, S ren
; APPLICANT: Bisgaard-Prantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-2

Query Match
 100.0%; Score 2720; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 H H N G T G T M M Q Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60
Db 1 H H N G T G T M M Q Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60

QY 61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V M M H K G G A D A T E N V L A V 120
Db 61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V M M H K G G A D A T E N V L A V 120

QY 121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180
Db 121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180

QY 181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N D G F R I D A V K H 240
Db 181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N D G F R I D A V K H 240

QY 241 I K Y S F T R D W L T H V R N A T G K E M F A V A E F W K N D L G A L E N Y L N K T N W N H S V F D V P L H Y N L Y N A 300
Db 241 I K Y S F T R D W L T H V R N A T G K E M F A V A E F W K N D L G A L E N Y L N K T N W N H S V F D V P L H Y N L Y N A 300

QY 301 S N S G G N Y D M A K L I N G T V V Q K H P M H A V T F V D N H D S Q P G E S L E S F V Q S W F K P L A Y A L I L T R E 360
Db 301 S N S G G N Y D M A K L I N G T V V Q K H P M H A V T F V D N H D S Q P G E S L E S F V Q S W F K P L A Y A L I L T R E 360

QY 361 Q G Y P S V F Y G D Y G I P T H S V P A M K A K I D P I L E A R Q N F A Y G T Q H D Y F D H N I I G W T R E G N T T 420
Db 361 Q G Y P S V F Y G D Y G I P T H S V P A M K A K I D P I L E A R Q N F A Y G T Q H D Y F D H N I I G W T R E G N T T 420

QY 421 H P N S G L A T I M S D G P G G E K M Y V Q N K A G Q V W H D I T G N K P G T V T I N A D G W A N F S V N G G S V S 480
Db 421 H P N S G L A T I M S D G P G G E K M Y V Q N K A G Q V W H D I T G N K P G T V T I N A D G W A N F S V N G G S V S 480

QY 481 I W V K R 485
Db 481 I W V K R 485

RESULT 7
US-09-193-068-8
; Sequence 8; Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjøluff, S ren
; APPLICANT: Bisgaard-Prantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-8

Query Match
 100.0%; Score 2720; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 H H N G T G T M M Q Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60
Db 1 H H N G T G T M M Q Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60

QY 61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V M M H K G G A D A T E N V L A V 120
Db 61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V M M H K G G A D A T E N V L A V 120

QY 121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180
Db 121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180

QY 181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N D G F R I D A V K H 240
Db 181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N D G F R I D A V K H 240

QY 241 I K Y S F T R D W L T H V R N A T G K E M F A V A E F W K N D L G A L E N Y L N K T N W N H S V F D V P L H Y N L Y N A 300
Db 241 I K Y S F T R D W L T H V R N A T G K E M F A V A E F W K N D L G A L E N Y L N K T N W N H S V F D V P L H Y N L Y N A 300

QY 301 S N S G G N Y D M A K L I N G T V V Q K H P M H A V T F V D N H D S Q P G E S L E S F V Q S W F K P L A Y A L I L T R E 360
Db 301 S N S G G N Y D M A K L I N G T V V Q K H P M H A V T F V D N H D S Q P G E S L E S F V Q S W F K P L A Y A L I L T R E 360

QY 361 Q G Y P S V F Y G D Y G I P T H S V P A M K A K I D P I L E A R Q N F A Y G T Q H D Y F D H N I I G W T R E G N T T 420
Db 361 Q G Y P S V F Y G D Y G I P T H S V P A M K A K I D P I L E A R Q N F A Y G T Q H D Y F D H N I I G W T R E G N T T 420

QY 421 H P N S G L A T I M S D G P G G E K M Y V Q N K A G Q V W H D I T G N K P G T V T I N A D G W A N F S V N G G S V S 480
Db 421 H P N S G L A T I M S D G P G G E K M Y V Q N K A G Q V W H D I T G N K P G T V T I N A D G W A N F S V N G G S V S 480

QY 481 I W V K R 485
Db 481 I W V K R 485
```



Db 241 IKYSFTRDLTHVRNATGKEMFAVAFWKNDLGALENYLNTKNWHSFVDFPLHYNLA 300  
Qy 301 SNSGGNDMAKLLNGTVVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTRE 360  
Db 301 SNSGGNDMAKLLNGTVVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTRE 360  
Qy 361 QGYPSVFYGDYIGPITHSVPAKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
Db 361 QGYPSVFYGDYIGPITHSVPAKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
Qy 421 HPNSGLATIMSDGPGGKWMYVQNKAGQVWHDDITGNKPGTGTINADGWANFVNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKWMYVQNKAGQVWHDDITGNKPGTGTINADGWANFVNGGSVS 480  
Qy 481 IWVKR 485  
Db 481 IWVKR 485

RESULT 10  
US-09-264-097-5  
; Sequence 5, Application US/09264097  
; Patent No. 6287826  
; GENERAL INFORMATION:  
; APPLICANT: Hendriksen, Hanne Vang  
; TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup  
; FILE REFERENCE: 5278.200-US  
; CURRENT APPLICATION NUMBER: US/09/264.097  
; CURRENT FILING DATE: 1999-03-08  
; EARLIER APPLICATION NUMBER: PA 0321/98  
; EARLIER FILING DATE: 1998-03-09  
; EARLIER APPLICATION NUMBER: 60/079,209  
; EARLIER FILING DATE: 1998-03-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus

US-09-264-097-5

Query Match 100.0%; Score 2720; DB 3; Length 485;  
Best Local Similarity 100.0%; Pred. No. 2.4e-232;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Db 1 HHNGTGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Qy 61 YDLYDLGEFNQKGTVRTKYTRQSLESIAHALKKNQVQVYGVVNMHKGADATENVLAV 120  
Db 61 YDLYDLGEFNQKGTVRTKYTRQSLESIAHALKKNQVQVYGVVNMHKGADATENVLAV 120  
Qy 121 EVNPNRNRQIESGDYITIAWTKFDFPGKNTYSDFKRWYHFDGVDWQSQRFQNRKYKF 180  
Db 121 EVNPNRNRQIESGDYITIAWTKFDFPGKNTYSDFKRWYHFDGVDWQSQRFQNRKYKF 180  
Qy 181 RGDGKAWDEVDSENGYDLYMTADVMDHPPEVNEIRRWGEWYTNLNDGFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGYDLYMTADVMDHPPEVNEIRRWGEWYTNLNDGFRIDAVKH 240  
Qy 241 IKYSFTRDLTHVRNATGKEMFAVAFWKNDLGALENYLNTKNWHSFVDFPLHYNLA 300  
Db 241 IKYSFTRDLTHVRNATGKEMFAVAFWKNDLGALENYLNTKNWHSFVDFPLHYNLA 300  
Qy 301 SNSGGNDMAKLLNGTVVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTRE 360  
Db 301 SNSGGNDMAKLLNGTVVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTRE 360  
Qy 361 QGYPSVFYGDYIGPITHSVPAKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420

Db 361 QGYPSVFYGDYIGPITHSVPAKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
Qy 421 HPNSGLATIMSDGPGGKWMYVQNKAGQVWHDDITGNKPGTGTINADGWANFVNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKWMYVQNKAGQVWHDDITGNKPGTGTINADGWANFVNGGSVS 480  
Qy 481 IWVKR 485  
Db 481 IWVKR 485

RESULT 11  
US-09-354-191A-2  
; Sequence 2, Application US/09354191A  
; Patent No. 6297038  
; GENERAL INFORMATION:  
; APPLICANT: Bisgard-Prantzen, Henrik  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Borcherdt, Torben Vedel  
; TITLE OF INVENTION: AMYLASE VARIANTS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.  
; STREET: 405 Lexington Avenue, Suite 6400  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/354,191A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/600,656  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 4318.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 867 0123  
; TELEFAX: 212 867 0298  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-09-354-191A-2

Query Match 100.0%; Score 2720; DB 3; Length 485;  
Best Local Similarity 100.0%; Pred. No. 2.4e-232;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Db 1 HHNGTGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Qy 61 YDLYDLGEFNQKGTVRTKYTRQSLESIAHALKKNQVQVYGVVNMHKGADATENVLAV 120  
Db 61 YDLYDLGEFNQKGTVRTKYTRQSLESIAHALKKNQVQVYGVVNMHKGADATENVLAV 120  
Qy 121 EVNPNRNRQIESGDYITIAWTKFDFPGKNTYSDFKRWYHFDGVDWQSQRFQNRKYKF 180  
Db 121 EVNPNRNRQIESGDYITIAWTKFDFPGKNTYSDFKRWYHFDGVDWQSQRFQNRKYKF 180

Qy 181 RGDGKAWDEVDSENGNYDYLMYADVDMDHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNYDYLMYADVDMDHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240  
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300  
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300  
Qy 301 SNSGNTDMAKLTNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
Db 301 SNSGNTDMAKLTNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
Qy 361 QGYPSEVFGDYGYGIPHTSVPAKAKIDPILLEARQNEAYGTOHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPSEVFGDYGYGIPHTSVPAKAKIDPILLEARQNEAYGTOHDYFDHNNIIGWTREGNTT 420  
Qy 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTVTINADGWANFVSNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTVTINADGWANFVSNGGSVS 480  
Qy 481 IWVKR 485  
Db 481 IWVKR 485  
RESULT 12  
US-09-734-2  
; Sequence 2, Application US/09290734  
; Patent No. 6361989  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Borchert, Torben Vedel  
; APPLICANT: Bisgard-Frantzen Henrik  
; APPLICANT: Outtrup, Helle  
; APPLICANT: Nielsen, Bjarne Ronfeldt  
; APPLICANT: Nielsen, Vibeke Skovgaard  
; APPLICANT: Hoeck, Lisbeth Hedegaard  
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants  
; FILE REFERENCE: 5276.400-US  
; CURRENT APPLICATION NUMBER: US/09/290,734  
; CURRENT FILING DATE: 1999-04-13  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-290-734-2

Query Match 100.0%; Score 2720; DB 4; Length 485;  
Best Local Similarity 100.0%; Pred. No. 2.4e-232;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 HNGTNGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60  
Qy 61 YDLVLDGEFNGKGTVRTKYGTRSQLESIAHALKNGVQVYGDVVMNHKGGADATENVLAV 120  
Db 61 YDLVLDGEFNGKGTVRTKYGTRSQLESIAHALKNGVQVYGDVVMNHKGGADATENVLAV 120  
Qy 121 EVNPNRNRQEISGDYTTIEAWTKFDPGCRGNTYSDFKRWYHFDGVDMDQSRQFNRIYKF 180  
Db 121 EVNPNRNRQEISGDYTTIEAWTKFDPGCRGNTYSDFKRWYHFDGVDMDQSRQFNRIYKF 180  
Qy 181 RGDGKAWDEVDSENGNYDYLMYADVDMDHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNYDYLMYADVDMDHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240  
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300  
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300  
Qy 301 SNSGNTDMAKLTNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
Db 301 SNSGNTDMAKLTNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
Qy 361 QGYPSEVFGDYGYGIPHTSVPAKAKIDPILLEARQNEAYGTOHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPSEVFGDYGYGIPHTSVPAKAKIDPILLEARQNEAYGTOHDYFDHNNIIGWTREGNTT 420

Qy 301 SNSGNTDMAKLTNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
Db 301 SNSGNTDMAKLTNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
Qy 361 QGYPSEVFGDYGYGIPHTSVPAKAKIDPILLEARQNEAYGTOHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPSEVFGDYGYGIPHTSVPAKAKIDPILLEARQNEAYGTOHDYFDHNNIIGWTREGNTT 420  
Qy 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTVTINADGWANFVSNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTVTINADGWANFVSNGGSVS 480  
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US-09-734-8  
; Sequence 8, Application US/09290734  
; Patent No. 6361989  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Borchert, Torben Vedel  
; APPLICANT: Bisgard-Frantzen Henrik  
; APPLICANT: Outtrup, Helle  
; APPLICANT: Nielsen, Bjarne Ronfeldt  
; APPLICANT: Nielsen, Vibeke Skovgaard  
; APPLICANT: Hoeck, Lisbeth Hedegaard  
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants  
; FILE REFERENCE: 5276.400-US  
; CURRENT APPLICATION NUMBER: US/09/290,734  
; CURRENT FILING DATE: 1999-04-13  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-290-734-8

Query Match 100.0%; Score 2720; DB 4; Length 485;  
Best Local Similarity 100.0%; Pred. No. 2.4e-232;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 HNGTNGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60  
Qy 61 YDLVLDGEFNGKGTVRTKYGTRSQLESIAHALKNGVQVYGDVVMNHKGGADATENVLAV 120  
Db 61 YDLVLDGEFNGKGTVRTKYGTRSQLESIAHALKNGVQVYGDVVMNHKGGADATENVLAV 120  
Qy 121 EVNPNRNRQEISGDYTTIEAWTKFDPGCRGNTYSDFKRWYHFDGVDMDQSRQFNRIYKF 180  
Db 121 EVNPNRNRQEISGDYTTIEAWTKFDPGCRGNTYSDFKRWYHFDGVDMDQSRQFNRIYKF 180  
Qy 181 RGDGKAWDEVDSENGNYDYLMYADVDMDHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNYDYLMYADVDMDHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240  
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300  
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300  
Qy 301 SNSGNTDMAKLTNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
Db 301 SNSGNTDMAKLTNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEFKPLAYALILTRE 360  
Qy 361 QGYPSEVFGDYGYGIPHTSVPAKAKIDPILLEARQNEAYGTOHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPSEVFGDYGYGIPHTSVPAKAKIDPILLEARQNEAYGTOHDYFDHNNIIGWTREGNTT 420

QY 421 HPNSGLATIMSDPGGKWMYVQNKAGQVWHDTGNKPGTGTINADGWANFSVNGSGVS 480  
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 QY 481 IWVKR 485  
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RESULT 14  
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 ; Sequence 3, Application US/09381687  
 ; Patent No. 6486113  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Borchert, Torben Vedel  
 ; APPLICANT: Bisgard-Frantzen Henrik  
 ; APPLICANT: Outtrup, Helle  
 ; APPLICANT: Nielsen, Bjarne Ronfeldt  
 ; APPLICANT: Nielsen, Vibeke Skovgaard  
 ; APPLICANT: Hoeck, Lisbeth Hedegaard  
 ; TITLE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants  
 ; FILE REFERENCE: 5276 400-US  
 ; CURRENT APPLICATION NUMBER: US/09/545,586  
 ; CURRENT FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: US/09/290,734  
 ; PRIOR FILING DATE: 1999-04-13  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 485  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus sp.  
 ; ORGANISM: Bacillus sp.  
 US-09-381-687-3

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 Job time : 16.0278 secs

RESULT 15  
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 ; Sequence 2, Application US/09545586  
 ; Patent No. 6528298  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Borchert, Torben Vedel  
 ; APPLICANT: Bisgard-Frantzen Henrik  
 ; APPLICANT: Outtrup, Helle  
 ; APPLICANT: Nielsen, Bjarne Ronfeldt  
 ; APPLICANT: Nielsen, Vibeke Skovgaard  
 ; APPLICANT: Hoeck, Lisbeth Hedegaard  
 ; TITLE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants  
 ; FILE REFERENCE: 5276 400-US  
 ; CURRENT APPLICATION NUMBER: US/09/545,586  
 ; CURRENT FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: US/09/290,734  
 ; PRIOR FILING DATE: 1999-04-13  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 485  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus sp.  
 ; ORGANISM: Bacillus sp.  
 US-09-545-586-2

Query Match 100.0%; Score 2720; DB 4; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-232;  
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 QY 121 EVNPNRNQIISGDYTIETAEWTKDFPGRGNTYSDFKRWYHFDGVDQDQSRQFQNRKYF 180  
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 QY 481 IWVKR 485



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.4478 Seconds  
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2920.093 Million cell updates/sec

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Perfect score: 2720  
Sequence: 1 HHNGTNGTMMQYFEWHLND.....ADGWANFVNGSGSVIWKV 485

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	2720	100.0	485 9	US-09-769-864-8 Sequence 8, Appli
3	2720	100.0	485 9	US-09-854-346-4 Sequence 4, Appli
4	2720	100.0	485 9	US-09-902-188A-2 Sequence 2, Appli
5	2720	100.0	485 9	US-09-918-543-4 Sequence 4, Appli
6	2720	100.0	485 9	US-09-795-211-2 Sequence 2, Appli
7	2720	100.0	485 10	US-09-925-576C-4 Sequence 4, Appli
8	2720	100.0	485 12	US-10-665-667-2 Sequence 2, Appli
9	2720	100.0	485 12	US-10-665-667-8 Sequence 8, Appli
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12	2720	100.0	485 12	US-10-327-837-8 Sequence 8, Appli
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18	2448	90.0	485 9	US-09-918-543-2 Sequence 2, Appli
19	2448	90.0	485 10	US-09-795-211-1 Sequence 1, Appli
20	2448	90.0	485 10	US-09-925-576C-2 Sequence 2, Appli
21	2448	90.0	485 12	US-10-665-667-1 Sequence 1, Appli
22	2448	90.0	485 12	US-10-665-667-7 Sequence 7, Appli
23	2448	90.0	485 12	US-10-025-648-1 Sequence 1, Appli
24	2448	90.0	485 12	US-10-327-837-1 Sequence 7, Appli
25	2448	90.0	485 12	US-10-327-837-7 Sequence 7, Appli
26	2448	90.0	485 14	US-10-184-771-12 Sequence 12, Appli
27	2448	90.0	485 16	US-10-477-725-2 Sequence 2, Appli
28	2448	89.7	516 9	US-09-986-676A-2 Sequence 2, Appli
29	2440	89.7	516 9	US-09-971-611-2 Sequence 2, Appli
30	2440	89.7	516 16	US-10-399-161-8 Sequence 8, Appli
31	2437	89.6	485 9	US-09-854-346-12 Sequence 12, Appli
32	2437	89.6	485 9	US-09-918-543-12 Sequence 12, Appli
33	2437	89.6	485 10	US-09-925-576C-12 Sequence 12, Appli
34	2437	89.6	485 12	US-10-327-837-24 Sequence 24, Appli
35	2437	89.6	485 12	US-10-327-837-26 Sequence 26, Appli
36	2437	89.6	485 14	US-10-209-812-5 Sequence 5, Appli
37	2437	89.6	485 16	US-10-477-725-12 Sequence 12, Appli
38	2430	89.3	516 16	US-10-343-212-2 Sequence 2, Appli
39	2414	88.8	485 9	US-09-769-864-6 Sequence 6, Appli
40	2414	88.8	485 9	US-09-854-346-13 Sequence 13, Appli
41	2414	88.8	485 9	US-09-902-188A-7 Sequence 7, Appli
42	2414	88.8	485 10	US-09-925-576C-13 Sequence 13, Appli
43	2414	88.8	485 12	US-10-665-667-6 Sequence 6, Appli
44	2414	88.8	485 12	US-10-025-648-7 Sequence 7, Appli
45	2414	88.8	485 12	US-10-327-837-6 Sequence 6, Appli

## ALIGNMENTS

RESULT 1  
US-09-769-864-2  
; Sequence 2, Application US/09769864  
; Patent No. US20010039253A1  
; GENERAL INFORMATION:  
; APPLICANT: Borchert, Torben V.  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Andersen, Carsten  
; APPLICANT: Nielsen, Bjarne  
; APPLICANT: Nissen, Torben L.  
; APPLICANT: Kjaerulff, Soren  
; TITLE OF INVENTION: Alpha-Amulase Mutants  
; FILE REFERENCE: 5368.200-US  
; CURRENT APPLICATION NUMBER: US/09/769,864  
; CURRENT FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/183,412  
; PRIOR FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-769-864-2

Query Match	100.0%;	Score 2720;	DB 9;	Length 485;
Best Local Similarity	100.0%;	Pred. No. 1.4e-243;		
Matches	485;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	HHNGTNGTMMQYFEWHLNDGNHWNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA	60	
Db	1	HHNGTNGTMMQYFEWHLNDGNHWNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA	60	
Qy	61	YDLVDLGEFNGKQVTRTKYGTTRSQLESIAHALKNGVQVGVVMMHKGADATENVLAV	120	
Db	61	YDLVDLGEFNGKQVTRTKYGTTRSQLESIAHALKNGVQVGVVMMHKGADATENVLAV	120	
Qy	121	EVFNERNQELSGDYTIEAWTKFDPGRGNTYSDFKRWYHFDGVDVDSRQFQNRYYKF	180	

Db 121 EVNPNRNRQISGDYTTIEAWTKFDPPGRGNTYSDFKRWYTHFDGWDQSRQFNRIYKF 180  
Qy 181 RGDGKAWDEVDSENGNDYLYMADVMDHPEVNNELRWGEWYTNLTNDGFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNDYLYMADVMDHPEVNNELRWGEWYTNLTNDGFRIDAVKH 240  
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHSHVFDVPLHYNLNA 300  
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHSHVFDVPLHYNLNA 300  
Qy 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEFKPLAYALLITRE 360  
Db 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEFKPLAYALLITRE 360  
Qy 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDIITGNKPGTGTVTINADGWFANFVSGSVS 480  
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDIITGNKPGTGTVTINADGWFANFVSGSVS 480  
Qy 481 IWVKR 485  
Db 481 IWVKR 485

RESULT 2

US-09-769-864-8  
; Sequence 8, Application US/09769864  
; Patent No. US20010039253A1  
; GENERAL INFORMATION:  
; APPLICANT: Borchert, Torben V.  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Andersen, Carsten  
; APPLICANT: Nielsen, Bjarne  
; APPLICANT: Nielsen, Torben I.  
; APPLICANT: Kjaerulff, Soren  
; TITLE OF INVENTION: Alpha-Amulase Mutants  
; FILE REFERENCE: 5368.200-US  
; CURRENT APPLICATION NUMBER: US/09/769, 864  
; CURRENT FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/183,412  
; PRIOR FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-769-864-8

Query Match 100.0%; Score 2720; DB 9; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1.4e-243;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Db 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Qy 61 YDLYDLGEFNGKGTVRTKYTRSQLESIAHALKNNGVQYVGVVMMHKGADATENVLAV 120  
Db 61 YDLYDLGEFNGKGTVRTKYTRSQLESIAHALKNNGVQYVGVVMMHKGADATENVLAV 120  
Qy 121 EVNPNRNRQISGDYTTIEAWTKFDPPGRGNTYSDFKRWYTHFDGWDQSRQFNRIYKF 180  
Db 121 EVNPNRNRQISGDYTTIEAWTKFDPPGRGNTYSDFKRWYTHFDGWDQSRQFNRIYKF 180  
Qy 181 RGDGKAWDEVDSENGNDYLYMADVMDHPEVNNELRWGEWYTNLTNDGFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNDYLYMADVMDHPEVNNELRWGEWYTNLTNDGFRIDAVKH 240

Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHSHVFDVPLHYNLNA 300  
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHSHVFDVPLHYNLNA 300  
Qy 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEFKPLAYALLITRE 360  
Db 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEFKPLAYALLITRE 360  
Qy 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDIITGNKPGTGTVTINADGWFANFVSGSVS 480  
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDIITGNKPGTGTVTINADGWFANFVSGSVS 480  
Qy 481 IWVKR 485  
Db 481 IWVKR 485

RESULT 3

US-09-854-346-4  
; Sequence 4, Application US/09854346  
; Patent No. US20020068352A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020068352A1ozymes A/S  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Jorgensen, Christel Thea  
; APPLICANT: Nielsen, Bjarne Ronfeldt  
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity  
; FILE REFERENCE: 6140.200-US  
; CURRENT APPLICATION NUMBER: US/09/854,346  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 4  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-854-346-4

Query Match 100.0%; Score 2720; DB 9; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1.4e-243;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Db 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60  
Qy 61 YDLYDLGEFNGKGTVRTKYTRSQLESIAHALKNNGVQYVGVVMMHKGADATENVLAV 120  
Db 61 YDLYDLGEFNGKGTVRTKYTRSQLESIAHALKNNGVQYVGVVMMHKGADATENVLAV 120  
Qy 121 EVNPNRNRQISGDYTTIEAWTKFDPPGRGNTYSDFKRWYTHFDGWDQSRQFNRIYKF 180  
Db 121 EVNPNRNRQISGDYTTIEAWTKFDPPGRGNTYSDFKRWYTHFDGWDQSRQFNRIYKF 180  
Qy 181 RGDGKAWDEVDSENGNDYLYMADVMDHPEVNNELRWGEWYTNLTNDGFRIDAVKH 240  
Db 181 RGDGKAWDEVDSENGNDYLYMADVMDHPEVNNELRWGEWYTNLTNDGFRIDAVKH 240  
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHSHVFDVPLHYNLNA 300  
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHSHVFDVPLHYNLNA 300  
Qy 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEFKPLAYALLITRE 360  
Db 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEFKPLAYALLITRE 360  
Qy 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTREGNTT 420  
Db 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTREGNTT 420



QY 361 QGYPSVFYGDYGYGIPTHSVPAWAKADIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
Db 361 QGYPSVFYGDYGYGIPTHSVPAWAKADIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
QY 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480  
QY 481 IWVKR 485  
Db 481 IWVKR 485  
RESULT 6  
US-09-795-211-2  
; Sequence 2, Application US/09795211  
; Publication No. US2002018226A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Kasturi, Chandrika  
; APPLICANT: Wandstrat, Mark E.  
; APPLICANT: Song, Brian X.  
; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZY  
; TITLE OF INVENTION: STABILITY  
; FILE REFERENCE: Detergent Composition  
; CURRENT APPLICATION NUMBER: US/09/795,211  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: alakaliphilic bacillus  
US-09-795-211-2  
Query Match 100.0%; Score 2720; DB 9; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1.4e-243;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKTSONDVGYGA 60  
Db 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKTSONDVGYGA 60  
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKNNGVQVYGVVNMHKGADATENVLAV 120  
Db 61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKNNGVQVYGVVNMHKGADATENVLAV 120  
QY 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKRWYTHFDGVDWDQSRQFNRIYKF 180  
Db 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKRWYTHFDGVDWDQSRQFNRIYKF 180  
QY 181 RGDKAWDEVDSENGNYDLYMTADVMDHPEVNVNLRWGEWYTNLNDGFRIDAVKH 240  
Db 181 RGDKAWDEVDSENGNYDLYMTADVMDHPEVNVNLRWGEWYTNLNDGFRIDAVKH 240  
QY 241 IKYSFTRDWLTHVRNATGKEMFAVEAFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300  
Db 241 IKYSFTRDWLTHVRNATGKEMFAVEAFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300  
QY 301 SNSGGNYDMAKLLNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360  
Db 301 SNSGGNYDMAKLLNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360  
QY 361 QGYPSVFYGDYGYGIPTHSVPAWAKADIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
Db 361 QGYPSVFYGDYGYGIPTHSVPAWAKADIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
QY 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480  
QY 481 IWVKR 485

Db 481 IWVKR 485  
RESULT 7  
US-09-925-576C-4  
; Sequence 4, Application US/09925576C  
; Publication No. US20030129718A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Carsten  
; APPLICANT: Borchert, Torben Vedel  
; APPLICANT: Nielsen, Bjarne Ronfeldt  
; TITLE OF INVENTION: Amylase Variants  
; FILE REFERENCE: 10004.204-US  
; CURRENT APPLICATION NUMBER: US/09/925,576C  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-925-576C-4  
Query Match 100.0%; Score 2720; DB 10; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1.4e-243;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKTSONDVGYGA 60  
Db 1 HNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKTSONDVGYGA 60  
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKNNGVQVYGVVNMHKGADATENVLAV 120  
Db 61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKNNGVQVYGVVNMHKGADATENVLAV 120  
QY 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKRWYTHFDGVDWDQSRQFNRIYKF 180  
Db 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKRWYTHFDGVDWDQSRQFNRIYKF 180  
QY 181 RGDKAWDEVDSENGNYDLYMTADVMDHPEVNVNLRWGEWYTNLNDGFRIDAVKH 240  
Db 181 RGDKAWDEVDSENGNYDLYMTADVMDHPEVNVNLRWGEWYTNLNDGFRIDAVKH 240  
QY 241 IKYSFTRDWLTHVRNATGKEMFAVEAFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300  
Db 241 IKYSFTRDWLTHVRNATGKEMFAVEAFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300  
QY 301 SNSGGNYDMAKLLNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360  
Db 301 SNSGGNYDMAKLLNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360  
QY 361 QGYPSVFYGDYGYGIPTHSVPAWAKADIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
Db 361 QGYPSVFYGDYGYGIPTHSVPAWAKADIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420  
QY 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480  
Db 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480  
QY 481 IWVKR 485  
Db 481 IWVKR 485  
RESULT 8  
US-10-665-667-2  
; Sequence 2, Application US/10665667  
; Publication No. US20040038368A1  
; GENERAL INFORMATION:  
; APPLICANT: Borchert, Torben V.  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Andersen, Carsten

```
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-665-667-2

Query Match      100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Qy 61 YDLYDLGEFNGKQTVRTKYGTRSOLESAIHALKKNQGVQYGVVMMHKGADATENVLAV 120
Db 61 YDLYDLGEFNGKQTVRTKYGTRSOLESAIHALKKNQGVQYGVVMMHKGADATENVLAV 120
Qy 121 EVNPNNRNQEISGDIYTIKFTFPGRGNTYSDFKWRWYHFDGVDWDQSRQFNRIYKF 180
Db 121 EVNPNNRNQEISGDIYTIKFTFPGRGNTYSDFKWRWYHFDGVDWDQSRQFNRIYKF 180
Qy 181 RGDKAWDEVDSENGNYDLYMADVDMHDPVNNELRRGWYTNLTLDGFRIDAVKH 240
Db 181 RGDKAWDEVDSENGNYDLYMADVDMHDPVNNELRRGWYTNLTLDGFRIDAVKH 240
Qy 241 IKYSFTFDLWTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHSHVDFVPLHYNLYNA 300
Db 241 IKYSFTFDLWTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHSHVDFVPLHYNLYNA 300
Qy 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Qy 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILKARONFAYGTHQHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILKARONFAYGTHQHDYFDHNNIIGWTREGNTT 420
Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGVTVTINADGWANFVSNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGVTVTINADGWANFVSNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 9
US-10-665-667-8
; Sequence 8, Application US/10665667
; Publication No. US20040039368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US

; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-665-667-8

Query Match      100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Qy 61 YDLYDLGEFNGKQTVRTKYGTRSOLESAIHALKKNQGVQYGVVMMHKGADATENVLAV 120
Db 61 YDLYDLGEFNGKQTVRTKYGTRSOLESAIHALKKNQGVQYGVVMMHKGADATENVLAV 120
Qy 121 EVNPNNRNQEISGDIYTIKFTFPGRGNTYSDFKWRWYHFDGVDWDQSRQFNRIYKF 180
Db 121 EVNPNNRNQEISGDIYTIKFTFPGRGNTYSDFKWRWYHFDGVDWDQSRQFNRIYKF 180
Qy 181 RGDKAWDEVDSENGNYDLYMADVDMHDPVNNELRRGWYTNLTLDGFRIDAVKH 240
Db 181 RGDKAWDEVDSENGNYDLYMADVDMHDPVNNELRRGWYTNLTLDGFRIDAVKH 240
Qy 241 IKYSFTFDLWTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHSHVDFVPLHYNLYNA 300
Db 241 IKYSFTFDLWTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHSHVDFVPLHYNLYNA 300
Qy 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Qy 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILKARONFAYGTHQHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILKARONFAYGTHQHDYFDHNNIIGWTREGNTT 420
Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGVTVTINADGWANFVSNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGVTVTINADGWANFVSNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 10
US-10-025-648-2
; Sequence 2, Application US/10025648
; Publication No. US20030064908A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/025,648  
 ; FILING DATE: 19-Dec-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/600,656  
 ; FILING DATE: 13-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lambiris, Elias J.  
 ; REGISTRATION NUMBER: 33,728  
 ; REFERENCE/DOCKET NUMBER: 4318.204-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212 867 0123  
 ; TELEFAX: 212 867 0298  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 485 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-025-648-2

Query Match 100.0%; Score 2720; DB 12; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-243;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHNGTGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60  
 DB 1 HHNGTGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60  
 QY 61 YDLYDLGFEFNKQGTVRTKYGTRSQLESIAHALKKNNGVQVYGDVVMNHKGGADATENVLAV 120  
 DB 61 YDLYDLGFEFNKQGTVRTKYGTRSQLESIAHALKKNNGVQVYGDVVMNHKGGADATENVLAV 120  
 QY 121 EVNPNNRNQISGDYTIETAWTKFDFPGRGNTYSDFKRWTHFPGVDWDQSQRFQNRKYKF 180  
 DB 121 EVNPNNRNQISGDYTIETAWTKFDFPGRGNTYSDFKRWTHFPGVDWDQSQRFQNRKYKF 180  
 QY 181 RGDKAWDEVDSENGNYDYLMTADVMDHPEVNNELRRWGEWYTTNLDGFRIDAVKH 240  
 DB 181 RGDKAWDEVDSENGNYDYLMTADVMDHPEVNNELRRWGEWYTTNLDGFRIDAVKH 240  
 QY 241 IKYSFTRDLWTHVRNATGKEMFAVAFWKNDLGALENLYNKTNNHNSVFDVPLHYNLYNA 300  
 DB 241 IKYSFTRDLWTHVRNATGKEMFAVAFWKNDLGALENLYNKTNNHNSVFDVPLHYNLYNA 300  
 QY 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTVDNHDSPQGESLESFVQSWFKPLAYALILTRE 360  
 DB 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTVDNHDSPQGESLESFVQSWFKPLAYALILTRE 360  
 QY 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILEARQNFAYGTQHDYFDHNNIIGWTRGNNT 420  
 DB 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILEARQNFAYGTQHDYFDHNNIIGWTRGNNT 420  
 QY 421 HPNSGLATIMSDGPGGKMWYQNKAGQVWHDIITGNKPGTGTINADGWANFSVNGGSVS 480  
 DB 421 HPNSGLATIMSDGPGGKMWYQNKAGQVWHDIITGNKPGTGTINADGWANFSVNGGSVS 480  
 QY 481 IWKVR 485  
 DB 481 IWKVR 485

RESULT 11  
 US-10-327-837-2  
 ; Sequence 2, Application US/10327837  
 ; Publication No. US20030211958A1

; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Borchert, Torben Vedel  
 ; APPLICANT: Bisgard-Frantzen Henrik  
 ; APPLICANT: Outtrup, Helle  
 ; APPLICANT: Nielsen, Bjarne Ronfeldt  
 ; APPLICANT: Nielsen, Vibeke Skovgaard  
 ; APPLICANT: Hoeck, Lisbeth Hedegaard  
 ; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants  
 ; FILE REFERENCE: 5276.400-US  
 ; CURRENT APPLICATION NUMBER: US/10/327,837  
 ; CURRENT FILING DATE: 2002-12-23  
 ; PRIOR APPLICATION NUMBER: US/09/290,734  
 ; PRIOR FILING DATE: 1999-04-13  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 485  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus sp.  
 US-10-327-837-2

Query Match 100.0%; Score 2720; DB 12; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-243;  
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHNGTGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60  
 DB 1 HHNGTGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60  
 QY 61 YDLYDLGFEFNKQGTVRTKYGTRSQLESIAHALKKNNGVQVYGDVVMNHKGGADATENVLAV 120  
 DB 61 YDLYDLGFEFNKQGTVRTKYGTRSQLESIAHALKKNNGVQVYGDVVMNHKGGADATENVLAV 120  
 QY 121 EVNPNNRNQISGDYTIETAWTKFDFPGRGNTYSDFKRWTHFPGVDWDQSQRFQNRKYKF 180  
 DB 121 EVNPNNRNQISGDYTIETAWTKFDFPGRGNTYSDFKRWTHFPGVDWDQSQRFQNRKYKF 180  
 QY 181 RGDKAWDEVDSENGNYDYLMTADVMDHPEVNNELRRWGEWYTTNLDGFRIDAVKH 240  
 DB 181 RGDKAWDEVDSENGNYDYLMTADVMDHPEVNNELRRWGEWYTTNLDGFRIDAVKH 240  
 QY 241 IKYSFTRDLWTHVRNATGKEMFAVAFWKNDLGALENLYNKTNNHNSVFDVPLHYNLYNA 300  
 DB 241 IKYSFTRDLWTHVRNATGKEMFAVAFWKNDLGALENLYNKTNNHNSVFDVPLHYNLYNA 300  
 QY 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTVDNHDSPQGESLESFVQSWFKPLAYALILTRE 360  
 DB 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTVDNHDSPQGESLESFVQSWFKPLAYALILTRE 360  
 QY 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILEARQNFAYGTQHDYFDHNNIIGWTRGNNT 420  
 DB 361 QGYPSVFYGDYGIPTHSVPAMKAKIDPILEARQNFAYGTQHDYFDHNNIIGWTRGNNT 420  
 QY 421 HPNSGLATIMSDGPGGKMWYQNKAGQVWHDIITGNKPGTGTINADGWANFSVNGGSVS 480  
 DB 421 HPNSGLATIMSDGPGGKMWYQNKAGQVWHDIITGNKPGTGTINADGWANFSVNGGSVS 480  
 QY 481 IWKVR 485  
 DB 481 IWKVR 485

RESULT 12  
 US-10-327-837-8  
 ; Sequence 8, Application US/10327837  
 ; Publication No. US20030211958A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Borchert, Torben Vedel  
 ; APPLICANT: Bisgard-Frantzen Henrik  
 ; APPLICANT: Outtrup, Helle  
 ; APPLICANT: Nielsen, Bjarne Ronfeldt

```
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-10-327-837-8

Query Match      100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60
Qy 61 YDYLDELFEFQKQGTVRTKYGTRSQLESIAIHALKKNQGVQVGDVVMNKHGGADATENVLAV 120
Db 61 YDYLDELFEFQKQGTVRTKYGTRSQLESIAIHALKKNQGVQVGDVVMNKHGGADATENVLAV 120
Qy 121 EVNPNRNRQEIISGDYTTIEAWTKFDFPGRGNTYSDFKRWYHFDGVDWQSQRFQNRYYKF 180
Db 121 EVNPNRNRQEIISGDYTTIEAWTKFDFPGRGNTYSDFKRWYHFDGVDWQSQRFQNRYYKF 180
Qy 181 RGDGKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240
Db 181 RGDGKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
Qy 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Qy 361 QGYPSVYGYDYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVYGYDYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420
Qy 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 13
US-10-477-725-4
; Sequence 4, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 4
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-10-477-725-4

Query Match      100.0%; Score 2720; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60
Qy 61 YDYLDELFEFQKQGTVRTKYGTRSQLESIAIHALKKNQGVQVGDVVMNKHGGADATENVLAV 120
Db 61 YDYLDELFEFQKQGTVRTKYGTRSQLESIAIHALKKNQGVQVGDVVMNKHGGADATENVLAV 120
Qy 121 EVNPNRNRQEIISGDYTTIEAWTKFDFPGRGNTYSDFKRWYHFDGVDWQSQRFQNRYYKF 180
Db 121 EVNPNRNRQEIISGDYTTIEAWTKFDFPGRGNTYSDFKRWYHFDGVDWQSQRFQNRYYKF 180
Qy 181 RGDGKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240
Db 181 RGDGKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
Qy 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Qy 361 QGYPSVYGYDYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVYGYDYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420
Qy 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 14
US-09-769-864-1
; Sequence 1, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
; US-09-769-864-1

Query Match      90.0%; Score 2448; DB 9; Length 485;
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Best Local Similarity 87.2%; Pred. No. 2.5e-218;
Matches 423; Conservative 36; Mismatches 26; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60

Qy 61 YDLVDLGEFNGKGTVRTKYGTRNQLQAASVTSKNGGIQVYGDVVMNHKGGADGTEI VNAV 120
Db 61 YDLVDLGEFNGKGTVRTKYGTRNQLQAASVTSKNGGIQVYGDVVMNHKGGADGTEI VNAV 120

Qy 121 EVNPNRNOEISGDYITIEAWTKFDPGRGNTYSDFKRWTHFDGVDWQSRQFONRIYKF 180
Db 121 EVNPNRNOEISGDYITIEAWTKFDPGRGNTYSDFKRWTHFDGVDWQSRQFONRIYKF 180

Qy 181 RGDGKAWDEVDSENGNYDLYMADVMDHPEVNNELRRWGEWYTNLTLDGPRIDAVKH 240
Db 181 RGDGKAWDEVDSENGNYDLYMADVMDHPEVNNELRRWGEWYTNLTLDGPRIDAVKH 240

Qy 241 IKYSFTRDMLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDMLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300

Qy 301 SNSGGYDMRNLNGSVVQKHPTAVTFVDNHDSPQGESLESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNLNGSVVQKHPTAVTFVDNHDSPQGESLESFVQWFKPLAYALVLTRE 360

Qy 361 QGYPVSFYGDYIGIPTHSVPAKAKIDPILAEARONFAYGTQHDYFDHNNIIGWTRGNTT 420
Db 361 QGYPVSFYGDYIGIPTHSVPAKAKIDPILAEARONFAYGTQHDYFDHNNIIGWTRGNTT 420

Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGTGTVTINADGMANFVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGTGTVTINADGMANFVNGGSVS 480

Qy 481 IWVKR 485
Db 481 VWVKQ 485

Search completed: October 7, 2004, 00:57:26
Job time : 55.4478 secs

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RESULT 15
US-09-769-864-7
; Sequence 7, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-769-864-7

Query Match 90.0%; Score 2448; DB 9; Length 485;
Best Local Similarity 87.2%; Pred. No. 2.5e-218;
Matches 423; Conservative 36; Mismatches 26; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 62.1733 Seconds  
(without alignments)  
2340.424 Million cell updates/sec

Title: US-09-925-576C-6

Perfect score: 2854

Sequence: 1 AAFNCTMQYFWYLPDDG.....TRPTGCFVWTEPRLVAMP 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2854	100.0	515	2	AAR72449
2	2854	100.0	515	2	AAW31406
3	2854	100.0	515	3	AAAY9770
4	2854	100.0	515	4	AAAY97547
5	2854	100.0	515	5	ABB06935
6	2854	100.0	515	5	AAU21251
7	2854	100.0	515	5	ABB47852
8	2854	100.0	515	5	ABB76588
9	2847	99.8	514	2	AAAR78269
10	2836	99.4	549	6	ABU03090
11	2832	99.2	549	6	ABU03084
12	2808	98.4	549	1	AAAP70338
13	2787	97.7	515	2	AAW31502
14	2787	97.7	515	2	AAW48263
15	2787	97.7	515	2	AAAY25153
16	2787	97.7	515	6	ABB99483
17	2783	97.5	559	1	AAAP70580
18	2780	97.4	514	2	AAW12955
19	2780	97.4	514	2	AAAY15417
20	2780	97.4	514	2	AAAY07383
21	2780	97.4	514	3	AAAY99604
22	2777	97.3	514	3	AAAY07389
23	2776	97.3	572	1	AAAP70579
24	2750	96.4	512	2	AAAY07388
25	2727.5	95.6	548	2	AAW39744

26	2727.5	95.6	548	2	AAAY01585
27	2727.5	95.6	548	4	AAAG5879
28	2456	86.1	550	6	ABU03091
29	2434	85.3	515	1	AAAP80575
30	2426	85.0	472	6	ABG70532
31	2426	85.0	472	6	ABU03082
32	2414	84.6	546	6	ABU03105
33	2410	84.4	615	6	ABU03102
34	2410	84.4	644	6	ABU03106
35	2402	84.2	564	6	ABU03098
36	1921	67.3	519	4	AAE09762
37	1921	67.3	519	4	AAE09763
38	1918.5	67.2	485	2	AAW12110
39	1917	67.2	519	4	AAE09764
40	1915.5	67.1	485	3	AAAB29367
41	1915.5	67.1	485	3	AAAB29311
42	1914.5	67.1	485	2	AAW12131
43	1913.5	67.0	485	3	AAAB29364
44	1913.5	67.0	485	3	AAAB29391
45	1912.5	67.0	485	2	AAW12117

ALIGNMENTS

RESULT 1

AAAR72449

ID AAR72449 standard; protein; 515 AA.

XX AAR72449;

XX

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 01-DEC-1995 (first entry)

XX

DE Bacillus stearothermophilus alpha amylase (mature protein).

XX

KW Alpha amylase; variant; enzyme; detergent; additive; dishwashing;

KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;

KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;

XX

OS Geobacillus stearothermophilus.

XX

PN WO9510603-A1.

XX

PD 20-APR-1995.

XX

PF 05-OCT-1994; 94WO-DK000370.

XX

PR 08-OCT-1993; 93DK-00001133.

XX

PR 02-FEB-1994; 94DK-00000140.

XX

PA (NOVO ) NOVO-NORDISK AS.

XX

PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Theillers M;

PI Van Der Zee P;

XX

XX WPI; 1995-161790/21.

DR N-PSDB; AAQ88068.

XX

PT New Bacillus derived alpha-amylase variants - having amino acid

PT modifications to improve washing and/or dishwashing performance.

XX

XX Claim 34; Page 11-12; 105pp; English.

PS

CC Variant alpha amylase enzymes which have improved washing and/or as

CC detergent additives. The enzymes have one or more amino acid residues

CC added, deleted or substituted. The variants can also be used for textile

CC desizing prior to scouring, bleaching and dyeing. The variants have

CC improved thermostability, acid/alkaline stability; low temperature

CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to

CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR

```
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 515 AA;

Query Match      100.0%; Score 2854; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFPNGTMMQYFEWLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYY 60
Db 1 AAFPNGTMMQYFEWLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYY 60

QY 61 DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMYYADVDFDHKGADGTEWDAVE 120
Db 61 DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMYYADVDFDHKGADGTEWDAVE 120

QY 121 VNPSDRNOEISGTQIOIQAWTKEFPGRCNTYSSFKRWYHDPDGDWDESRKLSRIYKFRG 180
Db 121 VNPSDRNOEISGTQIOIQAWTKEFPGRCNTYSSFKRWYHDPDGDWDESRKLSRIYKFRG 180

QY 181 IGKAWDWEVDTENGNYDYLMTADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240
Db 181 IGKAWDWEVDTENGNYDYLMTADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240

QY 241 FSFPDMLSYRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFFYTASK 300
Db 241 FSFPDMLSYRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFFYTASK 300

QY 301 SGGAFDMRTLMTNLMKDQPTLAVTFVNDHDTPEGQALQSWDPWFKPLAYAFILTRQEG 360
Db 301 SGGAFDMRTLMTNLMKDQPTLAVTFVNDHDTPEGQALQSWDPWFKPLAYAFILTRQEG 360

QY 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTREGGTEKP 420
Db 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDGPGGSKWYVGKQHAGKVFYDLTGNSRSDTVTINSDCGWGEFKVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKWYVGKQHAGKVFYDLTGNSRSDTVTINSDCGWGEFKVNGGSVSW 480

QY 481 VPRKTTVSTTIARPIITTRPWTGEFVRWTEPRLVAMP 515
Db 481 VPRKTTVSTTIARPIITTRPWTGEFVRWTEPRLVAMP 515

RESULT 2
AAW31406
ID AAW31406 standard; protein; 515 AA.
XX
AC AAW31406;
XX
DT 17-OCT-2003 (revised)
DT 11-MAY-1998 (first entry)
XX
DE Bacillus stearothermophilus Termamyl-like alpha-amylase.
XX
KW Termamyl; alpha-amylase; enzyme engineering; protein engineering; starch;
KW liquefaction; saccharification; sweetener; textile desizing;
KW detergent additive; ss.
XX
OS Geobacillus stearothermophilus.
XX
PN WO9741213-A1.
XX
PD 06-NOV-1997.
XX
PF 30-APR-1997; 97WO-DK000197.
XX
PR 30-APR-1996; 96DK-00000515.
PR 28-JUN-1996; 96DK-00000712.
PR 11-JUL-1996; 96DK-00000775.
PR 08-NOV-1996; 96DK-00001263.
```

```
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
FI Svendsen A, Borchert TV, Bisgard-Frantzen H;
XX
DR WPI; 1997-549718/50.
DR N-PSDB; AAV02473.
XX
PT Termamyl-like alpha-amylase variants with improved properties - e.g.
PT increased stability at low pH and low calcium, useful as detergent
PT additives and in industrial starch processing e.g. liquefaction.
XX
PS Disclosure; Page 86; 101pp; English.
XX
CC This protein comprises the Termamyl-like alpha-amylase of Bacillus
CC steartothermophilus. The invention relates to novel variants of Termamyl-
CC like alpha-amylases that have alpha-amylase activity and exhibit an
CC alteration in at least one property selected from: substrate specificity;
CC binding or cleavage pattern; thermal stability; pH/activity or
CC pH/stability profile; stability towards oxidation; Ca2+ dependency and
CC specific activity. The variant has one or more mutations from those
CC listed in the specification in relation to Bacillus licheniformis
CC Termamyl (see AAW31404). Also claimed are constructs comprising DNA
CC encoding the variant (see AAV02471-73), and recombinant expression
CC vectors and transformed cells containing the DNA. The Termamyl-like alpha
CC -amylase variant is useful as a detergent additive and can also be used
CC in industrial starch processing e.g. liquefaction (claimed) or
CC saccharification to produce sweeteners, and in textile desizing
CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 515 AA;
```

```
Query Match      100.0%; Score 2854; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFPNGTMMQYFEWLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYY 60
Db 1 AAFPNGTMMQYFEWLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYY 60

QY 61 DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMYYADVDFDHKGADGTEWDAVE 120
Db 61 DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMYYADVDFDHKGADGTEWDAVE 120

QY 121 VNPSDRNOEISGTQIOIQAWTKEFPGRCNTYSSFKRWYHDPDGDWDESRKLSRIYKFRG 180
Db 121 VNPSDRNOEISGTQIOIQAWTKEFPGRCNTYSSFKRWYHDPDGDWDESRKLSRIYKFRG 180

QY 181 IGKAWDWEVDTENGNYDYLMTADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240
Db 181 IGKAWDWEVDTENGNYDYLMTADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240

QY 241 FSFPDMLSYRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFFYTASK 300
Db 241 FSFPDMLSYRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFFYTASK 300

QY 301 SGGAFDMRTLMTNLMKDQPTLAVTFVNDHDTPEGQALQSWDPWFKPLAYAFILTRQEG 360
Db 301 SGGAFDMRTLMTNLMKDQPTLAVTFVNDHDTPEGQALQSWDPWFKPLAYAFILTRQEG 360

QY 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTREGGTEKP 420
Db 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDGPGGSKWYVGKQHAGKVFYDLTGNSRSDTVTINSDCGWGEFKVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKWYVGKQHAGKVFYDLTGNSRSDTVTINSDCGWGEFKVNGGSVSW 480

QY 481 VPRKTTVSTTIARPIITTRPWTGEFVRWTEPRLVAMP 515
Db 481 VPRKTTVSTTIARPIITTRPWTGEFVRWTEPRLVAMP 515
```

RESULT 3  
 ID AAY99770  
 AC AAY99770 standard; protein; 515 AA.  
 AC AAY99770;  
 DT 12-SEP-2003 (revised)  
 DT 04-SEP-2000 (first entry)  
 DE Bacillus stearothermophilus Termamyl-like alpha-amylase #2.  
 KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;  
 KW saccharification; muten; mutant; enzyme stability; hybrid.  
 OS Geobacillus stearothermophilus.  
 PN WC200029560-A1.  
 XX 25-MAY-2000.  
 XX 16-NOV-1999; 99WO-DK000628.  
 XX 16-NOV-1998; 98DK-00001495.  
 XX (NOVO ) NOVO-NORDISK AS.  
 PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;  
 DR WPI; 2000-38777/33.  
 DR N-PSDB; AAA48482.  
 PT Variant of parent termamyl-like alpha amylase useful for washing, textile  
 PT desizing and starch liquefaction, comprising alterations in one or more  
 PT solvent exposed amino acid residues.  
 XX Claim 8; Fig 1; 80pp; English.  
 CC The present sequence is a parent alpha-amylase from which mutants with  
 CC increased stability at acidic pH, low calcium concentration and high  
 CC temperatures have been derived. A variant may contain mutations in one or  
 CC more solvent exposed amino acid residues to increase the overall  
 CC hydrophobicity of the enzyme or the overall number of methyl groups in  
 CC the side chains of exposed residues may be increased. The mutations can  
 CC be incorporated by site-directed mutagenesis or by random mutagenesis. As  
 CC a result of their increased stability, the variants are suitable for the  
 CC industrial processing of starch, i.e. starch liquefaction and  
 CC saccharification. They may also be useful for washing, dishwashing and  
 CC textile desizing. Hybrid alpha-amylases comprising partial amino acid  
 CC sequences derived from two or more alpha-amylases have also been created  
 CC in order to increase enzyme stability. Note: According to the  
 CC specification, the present sequence and the sequence shown in AAY99604  
 CC are the same. (Updated on 12-SEP-2003 to standardise OS field)  
 XX Sequence 515 AA;  
 SQ Query Match 100.0%; Score 2854; DB 3; Length 515;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-246;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAPFNGTMOYFEWYLPDDGTLTKVANEANNLSLGLITALLWLPAYKGTSRSDVGYY 60  
 DB 1 AAPFNGTMOYFEWYLPDDGTLTKVANEANNLSLGLITALLWLPAYKGTSRSDVGYY 60  
 QY 61 DLVDLGEFNGKGTVRTKYGKCAQVLOIAAHAGMOVYADVDFDHKGADGTSEWDAVE 120  
 DB 61 DLVDLGEFNGKGTVRTKYGKCAQVLOIAAHAGMOVYADVDFDHKGADGTSEWDAVE 120  
 QY 121 VNPSDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 DB 121 VNPSDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 QY 181 IGKAWDEVDTEGNGDYLYADLMDHPEVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240  
 DB 181 IGKAWDEVDTEGNGDYLYADLMDHPEVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240

Db 181 IGKAWDEVDTEGNGDYLYADLMDHPEVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240  
 QY 241 FSFFPDWLSYVRSQTGKPLFTVGEYMSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300  
 Db 241 FSFFPDWLSYVRSQTGKPLFTVGEYMSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300  
 QY 301 SGGAFDMRTLMTNLTMLKDOPTLAVTFVDNHDTEPGQALQSWVDWPKFLAYAFILTROEG 360  
 Db 301 SGGAFDMRTLMTNLTMLKDOPTLAVTFVDNHDTEPGQALQSWVDWPKFLAYAFILTROEG 360  
 QY 361 YPCVFYGDYGIQYNIPLSKSIDPLLIARRDYAVGTQHDYLDHSDIIGWTREGGTEKP 420  
 Db 361 YPCVFYGDYGIQYNIPLSKSIDPLLIARRDYAVGTQHDYLDHSDIIGWTREGGTEKP 420  
 QY 421 GSGLAALITDPCGSKWYVGVKQHAGKVFDLTGNRSDTVTIINSDGMEFKVNGGSVSW 480  
 Db 421 GSGLAALITDPCGSKWYVGVKQHAGKVFDLTGNRSDTVTIINSDGMEFKVNGGSVSW 480  
 QY 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515  
 Db 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515

RESULT 4  
 ID AAY97547 standard; protein; 515 AA.  
 AC AAY97547;  
 DT 11-SEP-2003 (revised)  
 DT 12-FEB-2001 (first entry)  
 DE B. stearothermophilus termamyl-like alpha amylase.  
 XX Termamyl-like alpha-amylase; variant; starch liquefaction; fuel;  
 KW detergent composition; laundry cleaning composition; ethanol production;  
 KW dish washing cleaning composition; hard surface cleaning composition;  
 KW industrial ethanol production; textile desizing.  
 OS Geobacillus stearothermophilus.  
 PN WC200060059-A2.  
 XX 12-OCT-2000.  
 XX 28-MAR-2000; 2000WO-DK000148.  
 XX 30-MAR-1999; 99DK-00000437.  
 XX (NOVO ) NOVO NORDISK AS.  
 PI Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;  
 PI Kjaerulff S;  
 DR WPI; 2001-015656/02.  
 DR N-PSDB; AAA37851.  
 PT New variants of parent Termamyl-like alpha-amylase, useful in starch  
 PT liquefaction, in detergent compositions and in ethanol production,  
 PT exhibit altered cleavage pattern relative to the parent.  
 XX Claim 17; Page 69-70; 78pp; English.  
 PS This sequence represents a termamyl-like alpha amylase. The invention  
 CC relates to a variant (I) of parent Termamyl-like alpha-amylase comprising  
 CC alteration at one or more of the positions W13, G48, T49, S50, Q51, A52,  
 CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (I)  
 CC are independently an insertion of an amino acid downstream of the amino  
 CC acid which occupies the position of deletion or substitution of the amino  
 CC acid which occupies the position with a different amino acid. The variant  
 CC has alpha-amylase activity. (I) or compositions containing it are useful  
 CC in starch liquefaction, in detergent compositions such as laundry, dish  
 CC washing and hard surface cleaning compositions, ethanol production such

CC as fuel, drinking and industrial ethanol production, desizing of  
CC textiles, fabrics or garments. (I) exhibits a reduced capability of  
CC cleaving a substrate close to the branching point, and further exhibits  
CC improved substrate specificity and/or improved specific activity relative  
CC to the parent alpha-amylase. (Updated on 11-SEP-2003 to standardise OS  
CC field)  
XX  
SQ Sequence 515 AA;

Query Match 100.0%; Score 2854; DB 4; Length 515;  
Best Local Similarity 100.0%; Pred. No. 7.4e-246;  
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLTKVANEANNSLGLTALWLPAYKGTSRSDVGYGVY 60  
DB 1 AAFNGTMMQYFEWYLPDDGTLTKVANEANNSLGLTALWLPAYKGTSRSDVGYGVY 60  
QY 61 DLYDLGEFNQKGTVRTKYGTKAQYLQALQAAHAAGMOMVYADVDFDHKGADGTWDAVE 120  
DB 61 DLYDLGEFNQKGTVRTKYGTKAQYLQALQAAHAAGMOMVYADVDFDHKGADGTWDAVE 120  
QY 121 VNPSDRNQEISGTQYQIAWTKEFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
DB 121 VNPSDRNQEISGTQYQIAWTKEFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
QY 181 IGKAWDEVDTEGNGYDLYMTADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240  
DB 181 IGKAWDEVDTEGNGYDLYMTADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240  
QY 241 FSFPFDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGDTMSLFDAPLHNKFTYASK 300  
DB 241 FSFPFDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGDTMSLFDAPLHNKFTYASK 300  
QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
DB 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
QY 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
DB 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
QY 421 GSGLAALITDGPGGSKWYVGKQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480  
DB 421 GSGLAALITDGPGGSKWYVGKQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480  
QY 481 VPRKTTVSTIARPTTTPWTGEFVRWTEPRLVAMP 515  
DB 481 VPRKTTVSTIARPTTTPWTGEFVRWTEPRLVAMP 515

RESULT 5  
ABB06935  
ID ABB06935 standard; protein; 515 AA.  
XX  
AC ABB06935;  
XX  
AC ABB06935;  
XX  
DT 29-AUG-2003 (revised)  
DT 19-JUN-2002 (first entry)  
XX  
XX B. steaerothermophilus termamyl-like alpha-amylase protein SEQ ID NO:6.  
XX  
XX Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;  
KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;  
KW washing; sweetener; ethanol; starch.  
XX  
XX Geobacillus steaerothermophilus.  
XX  
XX WO200166712-A2.  
XX  
XX 13-SEP-2001.  
XX  
XX 07-MAR-2001; 2001WO-DK000144.  
XX

PR 08-MAR-2000; 2000DK-000003176.  
PR 15-MAR-2000; 2000US-0189857P.  
PR 23-FEB-2001; 2001DK-00000303.  
PR 26-FEB-2001; 2001US-0271382P.  
XX  
PA (NOVO ) NOVOZYMES AS.  
XX  
XX Andersen C, Borchert TV, Nielsen BR;  
PI  
XX WPI; 2002-239612/29.  
DR N-PSDB; ABL50566.  
XX  
PT Novel variant of parent termamyl-like alpha-amylase useful as a component  
PT in washing and dishwashing compositions, for textile desizing, for starch  
PT liquefaction, and for producing sweeteners and ethanol from starch.  
XX  
PS Claim 8; Page 138-139; 153pp; English.

CC The present invention describes a variant of a parent termamyl-like alpha  
CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more  
CC positions of a group of 31 possible amino acid positions. The alteration  
CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,  
CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,  
CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,  
CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for  
CC washing and/or dishwashing, textile desizing, and starch liquefaction.  
CC (I) is useful as a component in hard surface cleaning detergent  
CC composition, and for producing sweeteners and ethanol from starch. (I)  
CC has altered solubility, preferably increased solubility, in particular  
CC under washing, dish washing or hard surface cleaning conditions. The  
CC present sequence represents a Bacillus steaerothermophilus termamyl-like  
CC alpha-amylase which is used in the exemplification of the present  
CC invention. (Updated on 29-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 515 AA;

Query Match 100.0%; Score 2854; DB 5; Length 515;  
Best Local Similarity 100.0%; Pred. No. 7.4e-246;  
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLTKVANEANNSLGLTALWLPAYKGTSRSDVGYGVY 60  
DB 1 AAFNGTMMQYFEWYLPDDGTLTKVANEANNSLGLTALWLPAYKGTSRSDVGYGVY 60  
QY 61 DLYDLGEFNQKGTVRTKYGTKAQYLQALQAAHAAGMOMVYADVDFDHKGADGTWDAVE 120  
DB 61 DLYDLGEFNQKGTVRTKYGTKAQYLQALQAAHAAGMOMVYADVDFDHKGADGTWDAVE 120  
QY 121 VNPSDRNQEISGTQYQIAWTKEFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
DB 121 VNPSDRNQEISGTQYQIAWTKEFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
QY 181 IGKAWDEVDTEGNGYDLYMTADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240  
DB 181 IGKAWDEVDTEGNGYDLYMTADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240  
QY 241 FSFPFDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGDTMSLFDAPLHNKFTYASK 300  
DB 241 FSFPFDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGDTMSLFDAPLHNKFTYASK 300  
QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
DB 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
QY 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
DB 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
QY 421 GSGLAALITDGPGGSKWYVGKQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480  
DB 421 GSGLAALITDGPGGSKWYVGKQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480  
QY 481 VPRKTTVSTIARPTTTPWTGEFVRWTEPRLVAMP 515

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Db 481 VPRKTTVSTIARPIITRPWTGFEVVRWTEPRLVAMP 515
|||||
RESULT 6
AAU12151
ID AAU12151 standard; protein; 515 AA.
AC AAU12151.
XX
XX 29-AUG-2003 (revised)
DT 09-APR-2002 (first entry)
XX
DE Bacillus TERMAMYL-like alpha-amylase BSG.
XX
XX TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
KW amylopectin; limit dextrin; NOVAMYL; BSG.
XX
OS Geobacillus stearothermophilus.
XX
XX WO200188107-A2.
XX
XX 22-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-DK000323.
XX
XX 12-MAY-2000; 2000DK-00000779.
XX
XX (NOVO ) NOVOZYMES AS.
XX
XX Svendsen A, Jorgensen CT, Nielsen BR;
XX
XX WPI; 2002-106123/14.
XX
XX N-PSDB; AAS20024.
XX
XX New variant of parent Termamyl-like alpha-amylase for use as a component
PT in washing and dishwashing compositions, for textile desizing, for starch
PT liquefaction, and for producing sweeteners and ethanol from starch.
XX
XX Claim 5; Fig 1; 84pp; English.
XX
XX The invention relates to a variant of parent TERMAMYL-like alpha- amylase
CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
CC or at position 234, where the variant has alpha-amylase activity and each
CC position corresponds to a position of a parent Termamyl-like alpha-
CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
CC of 483 amino acids, given in specification. The variant alpha- amylase, a
CC detergent additive comprising the variant or a detergent composition
CC comprising the variant, is useful for washing and/or dishwashing or
CC textile desizing. The alpha-amylase is useful for starch liquefaction or
CC ethanol production and as a component in a hard surface cleaning
CC detergent composition, and for producing sweeteners from starch. The
CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
CC branch linkage cleavage activity of amylopectin or a limit dextrin
CC prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
CC natural variant of the TERMAMYL alpha-amylase, BSG. (Updated on 29-AUG-
CC 2003 to standardise OS field)
XX
XX SQ Sequence 515 AA;
XX
Query Match 100.0%; Score 2854; DB 5; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 AAPNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALTALWLPAYKGTSRSDVGXGVY 60
Db 1 AAPNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALTALWLPAYKGTSRSDVGXGVY 60
XX
XX 61 DLYDLGFEFNQKGTVRTKYGKAQYLQAIQAARAGMOMVYADVPFDHKGADGTETWDAVE 120
QY 61 DLYDLGFEFNQKGTVRTKYGKAQYLQAIQAARAGMOMVYADVPFDHKGADGTETWDAVE 120
Db 61 DLYDLGFEFNQKGTVRTKYGKAQYLQAIQAARAGMOMVYADVPFDHKGADGTETWDAVE 120

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CC producing a maltodextrin or glucose syrup, by treating starch with a pre-oxidized alpha-amylase until a product with a DE between 5-45 has been provided and/or until a product with a molecular weight of between 5-30 kDa has been provided. The product comprises a maltodextrin with a DE of 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The alpha amylase is useful for producing a maltodextrin or glucose syrup, where the glucose syrup is useful as an ingredient in food, feed or pharmaceuticals. Glucose syrup is useful in confectionery such as candies, beverages such as isotonic drinks, bakery such as cereal bars, dairy and ice cream such as coffee whiteners, conventional foods such as salad dressings, and food ingredients and preparations such as cured meat, fermented meat, spices and seasoning encapsulated flavours. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 515 AA;

Query Match 100.0%; Score 2854; DB 5; Length 515;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-246;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLMTKVANEANLSSLGITALLWLPAYKGTSDVGYGY 60  
 DB 1 AAPFNGTMMQYFEWYLPDDGTLMTKVANEANLSSLGITALLWLPAYKGTSDVGYGY 60

QY 61 DLYDLGEFNGKGTVRTKYGTQAQYLOAIQAAHAAGMQYADVDFHKGADGTEWDAVE 120  
 DB 61 DLYDLGEFNGKGTVRTKYGTQAQYLOAIQAAHAAGMQYADVDFHKGADGTEWDAVE 120

QY 121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 DB 121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180

QY 181 IGKAWDWEVDTEGNGYDYLMDHDPVETLKNWGWYVNTTNDGFRDLDAVKHIK 240  
 DB 181 IGKAWDWEVDTEGNGYDYLMDHDPVETLKNWGWYVNTTNDGFRDLDAVKHIK 240

QY 241 FSPFPDMLSVRSQTGKPLFTVGEYNSYDINKLHNYITKTGDTMSLFDAPLHNKFTASK 300  
 DB 241 FSPFPDMLSVRSQTGKPLFTVGEYNSYDINKLHNYITKTGDTMSLFDAPLHNKFTASK 300

QY 301 SGGAFTMRTLTMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPPWPKLAYAFILTRQEG 360  
 DB 301 SGGAFTMRTLTMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPPWPKLAYAFILTRQEG 360

QY 361 YPCVFYDGYGIPQYNIPSLKSIDPLLIARRDYAGTQHDYLDHSDIIGWTREGGTEKP 420  
 DB 361 YPCVFYDGYGIPQYNIPSLKSIDPLLIARRDYAGTQHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDGPCKGSKWYVKGQHAGKVFDYDLTGNRSDTITNSDGMGEFKVNGGSVW 480  
 DB 421 GSGLAALITDGPCKGSKWYVKGQHAGKVFDYDLTGNRSDTITNSDGMGEFKVNGGSVW 480

QY 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRLVAMP 515  
 DB 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRLVAMP 515

RESULT 8  
 ABB76588  
 ID ABB76588 standard; protein; 515 AA.  
 XX  
 AC ABB76588;  
 XX  
 XX 29-AUG-2003 (revised)  
 DT 19-AUG-2002 (first entry)  
 XX  
 XX Termamyl-like-alpha-amylase #3.  
 DE  
 XX Termamyl; alpha amylase; starch liquefaction; ethanol production;  
 KW textile desizing; detergent; enzyme.  
 XX  
 OS Geobacillus stearothermophilus.

PN WO200210355-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 XX 12-JUL-2001; 2001WO-DK000488.  
 XX  
 PR 01-AUG-2000; 2000DK-00001160.  
 PR 12-SEP-2000; 2000DK-00001354.  
 PR 10-NOV-2000; 2000DK-00001687.  
 PR 26-APR-2001; 2001DK-00000655.  
 XX  
 PA (NOVO ) NOVOZYMES AS.  
 XX  
 PI Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;  
 XX  
 DR WPI; 2002-280633/32.  
 DR N-PSDB; ABL96209.  
 XX  
 XX Variant of parent Termamyl-like alpha amylase, useful in detergent compositions, for starch liquefaction, ethanol production, washing and/or dish washing, and textile desizing.  
 PT  
 PT Claim 4; Fig 5; 90pp; English.  
 PS  
 XX This invention relates to variants of a parent Termamyl-like alpha-amylases. These are used for starch liquefaction, ethanol production, detergent, and textile desizing. The amylases have altered stability, particularly at high temperatures from 70-120plusOC and low pH in the range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-amylase. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 515 AA;  
 Query Match 100.0%; Score 2854; DB 5; Length 515;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-246;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLMTKVANEANLSSLGITALLWLPAYKGTSDVGYGY 60  
 DB 1 AAPFNGTMMQYFEWYLPDDGTLMTKVANEANLSSLGITALLWLPAYKGTSDVGYGY 60

QY 61 DLYDLGEFNGKGTVRTKYGTQAQYLOAIQAAHAAGMQYADVDFHKGADGTEWDAVE 120  
 DB 61 DLYDLGEFNGKGTVRTKYGTQAQYLOAIQAAHAAGMQYADVDFHKGADGTEWDAVE 120

QY 121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 DB 121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180

QY 181 IGKAWDWEVDTEGNGYDYLMDHDPVETLKNWGWYVNTTNDGFRDLDAVKHIK 240  
 DB 181 IGKAWDWEVDTEGNGYDYLMDHDPVETLKNWGWYVNTTNDGFRDLDAVKHIK 240

QY 241 FSPFPDMLSVRSQTGKPLFTVGEYNSYDINKLHNYITKTGDTMSLFDAPLHNKFTASK 300  
 DB 241 FSPFPDMLSVRSQTGKPLFTVGEYNSYDINKLHNYITKTGDTMSLFDAPLHNKFTASK 300

QY 301 SGGAFTMRTLTMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPPWPKLAYAFILTRQEG 360  
 DB 301 SGGAFTMRTLTMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPPWPKLAYAFILTRQEG 360

QY 361 YPCVFYDGYGIPQYNIPSLKSIDPLLIARRDYAGTQHDYLDHSDIIGWTREGGTEKP 420  
 DB 361 YPCVFYDGYGIPQYNIPSLKSIDPLLIARRDYAGTQHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDGPCKGSKWYVKGQHAGKVFDYDLTGNRSDTITNSDGMGEFKVNGGSVW 480  
 DB 421 GSGLAALITDGPCKGSKWYVKGQHAGKVFDYDLTGNRSDTITNSDGMGEFKVNGGSVW 480

QY 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRLVAMP 515  
 DB 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRLVAMP 515

RESULT 9	
AA78269	
ID	AA78269 standard; protein; 514 AA.
XX	
AC	AA78269;
XX	
DT	16-OCT-2003 (revised)
DT	17-JAN-1996 (first entry)
XX	
DE	Bacillus stearothermophilus alpha amylase (mature protein).
XX	
KW	Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
KW	thermostable; methionine; Bacillus licheniformis;
KW	Bacillus amyloliquefaciens; Bacillus stearothermophilus.
XX	
OS	Geobacillus stearothermophilus.
XX	
PN	W09521247-A1.
XX	
PD	10-AUG-1995.
XX	
PF	05-OCT-1994; 94WO-DK000371.
XX	
PR	02-FEB-1994; 94DK-00000141.
XX	
PA	(NOVO ) NOVO-NORDISK AS.
XX	
PI	Toft AH, Marcher D, Pedersen HH, Nilsen TE;
XX	
DR	WPI; 1995-283767/37.
DR	N-PSDB; AAQ95033.
XX	
PT	Use of an oxidation stable alpha-amylase - for simultaneous desizing and
PT	bleaching or scouring of fabrics contg. starch or starch derivs.
XX	
PS	Claim 8; Page 25; 37pp; English.
XX	
CC	Oxidation stable alpha amylases can be used for the simultaneous desizing
CC	and bleaching or scouring of a fabric comprising starch or starch
CC	derivatives. They exhibit a better heat stability, especially in the
CC	presence of oxidising agents. They are obtained from a parent alpha
CC	amylase by replacing one or more methionine residues with any amino acid
CC	different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
CC	Asp. The parent alpha amylase is derived from a Bacillus species. This
CC	sequence is the wild type (unmodified) alpha amylase. (Updated on 16-OCT-
CC	2003 to standardise OS field)
XX	
SQ	Sequence 514 AA;
Query Match	99.8%; Score 2847; DB 2; Length 514;
Best Local Similarity	100.0%; Pred. No. 3.le-245;
Matches 514; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 AAPFNGTMMQYFEWLPDDGLTWKVAEANNLSLGLTALWLPAYKGTGRSDVGVGY 60
Db	1 AAPFNGTMMQYFEWLPDDGLTWKVAEANNLSLGLTALWLPAYKGTGRSDVGVGY 60
Qy	61 DLYDLGEFNQGTVRTKYGTAKYLAQIAAHAAGMOMVYADVDFDHKGAGDGTWVDAVE 120
Db	61 DLYDLGEFNQGTVRTKYGTAKYLAQIAAHAAGMOMVYADVDFDHKGAGDGTWVDAVE 120
Qy	121 VNPDRNQEISGTVQIQAWTFDPFGNGNTYSSFKRWYHFDGVNDWDSRKLRIYKPRG 180
Db	121 VNPDRNQEISGTVQIQAWTFDPFGNGNTYSSFKRWYHFDGVNDWDSRKLRIYKPRG 180
Qy	181 IGKAWDEVDTEGNYDYLWADLMDHPVVTELKNGKVVNTTIDGFRDLDAVKHK 240
Db	181 IGKAWDEVDTEGNYDYLWADLMDHPVVTELKNGKVVNTTIDGFRDLDAVKHK 240
Qy	241 FSFFPDMLSVRSQTKGLFTVGEYSYDINKLHNYITKDTGTSLSFDAPLHNKFTYASK 300
Db	241 FSFFPDMLSVRSQTKGLFTVGEYSYDINKLHNYITKDTGTSLSFDAPLHNKFTYASK 300

Qy	301 SGAFAFDMRTLMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db	301 SGAFAFDMRTLMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Qy	361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYCTQHDYLDHSDIIGWTREGGTEKP 420
Db	361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYCTQHDYLDHSDIIGWTREGGTEKP 420
Qy	421 GSGLAALITDGPGGSKMYYGKHAGKVFYDLTGNRSDTVTINSDGMEFKVNGSGSVVW 480
Db	421 GSGLAALITDGPGGSKMYYGKHAGKVFYDLTGNRSDTVTINSDGMEFKVNGSGSVVW 480
Qy	481 VPRKTTVSTIARPTTTPWTGCFVVRWTEPRLVAW 514
Db	481 VPRKTTVSTIARPTTTPWTGCFVVRWTEPRLVAW 514
RESULT 10	
ABU03090	
ID	ABU03090 standard; protein; 549 AA.
XX	
AC	ABU03090;
XX	
DT	21-JAN-2003 (first entry)
XX	
DE	Alpha amylase polypeptide #51.
XX	
KW	Alpha amylase; enzyme; starch linkage hydrolysis; starch liquefaction;
KW	starch breakdown catalysis; textile desizing; lignocellulosic fibre;
KW	enzymatic de-inking; recycled paper; high-maltose syrup; dough;
KW	high glucose syrup; corn-wet milling process; detergent; baking process;
KW	beverage; oil field; fuel ethanol; brewing process; staling;
KW	starch modification.
XX	
OS	Unidentified.
XX	
PN	W0200268589-A2.
XX	
PD	06-SEP-2002.
XX	
PF	21-FEB-2002; 2002WO-US005068.
XX	
PR	21-FEB-2001; 2001US-0270495P.
PR	21-FEB-2001; 2001US-0270496P.
PR	14-MAY-2001; 2001US-0291122P.
XX	
PA	(DIVE-) DIVERSA CORP.
XX	
PI	Callen W, Richardson T, Frey G;
XX	
DR	WPI; 2003-018656/01.
DR	N-PSDB; ABX08461.
XX	
PT	Novel purified polypeptide with alpha-amylase activity, useful e.g. for
PT	liquefying starch, for textile desizing, for treating lignocellulosic
PT	fibers, and for producing high-maltose or high-glucose syrup.
XX	
PS	Claim 30; Fig 16; 301pp; English.
XX	
CC	The invention relates to a purified polypeptide with alpha-amylase
CC	activity and the polynucleotide encoding it. The polypeptide is useful
CC	for hydrolysing starch linkages, for catalysing the breakdown of a
CC	starch, for modifying small molecules, for liquefying starch, for washing
CC	an object, for textile desizing, for treating lignocellulosic fibers, for
CC	improving fibre properties, for enzymatic de-inking of recycled paper
CC	pulp, for producing a high-maltose or high-glucose syrup or a mixed
CC	syrup, and for increasing the flow of production fluids from a
CC	subterranean formation by removing a viscous, starch-containing, damaging
CC	fluid formed during production operations and found within the
CC	subterranean formation which surrounds a completed well bore. The
CC	polypeptide is also useful for preparing a dough or a baked product
CC	prepared from the dough and in corn-wet milling processes, detergents,

CC baking processes, beverages, oil fields (fuel ethanol), brewing processes  
CC and starch modification in the paper and pulp industry, for removing  
CC starch containing stains from a material and for reducing staling of  
CC bakery products. Sequences ABU03040-ABU03144 represent alpha amylase  
CC polypeptides of the invention  
XX  
SQ Sequence 549 AA;  
  
Query Match 99.4%; Score 2836; DB 6; Length 549;  
Best Local Similarity 99.4%; Pred. No. 3.3e-244;  
Matches 512; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYY 60  
Db 35 AAPFNGTMQYFEWYLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYY 94  
  
Qy 61 DLYDLGEFNQKGTVRTKYGTAKYQLOAQIAHAAGMOYADVDFHKGADGTWDAVE 120  
Db 95 DLYDLGEFNQKGTVRTKYGTAKYQLOAQIAHAAGMOYADVDFHKGADGTWDAVE 154  
  
Qy 121 VNPSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180  
Db 155 VNPSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 214  
  
Qy 181 IGKAWDWEVDTENGNYDYLWADLMDHPEVVTTELKNWGWYNTTIDGFRDLDAVKHIK 240  
Db 215 IGKAWDWEVDTENGNYDYLWADLMDHPEVVTTELKNWGWYNTTIDGFRDLDAVKHIK 274  
  
Qy 241 FSFPFDWLSVRSQTKPLFTVGEWYSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 300  
Db 275 FSFPFDWLSVRSQTKPLFTVGEWYSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 334  
  
Qy 301 SGGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGALQSWDVPWFKPLAYAFILTRQEG 360  
Db 335 SGGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGALQSWDVPWFKPLAYAFILTRQEG 394  
  
Qy 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 420  
Db 395 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 454  
  
Qy 421 GSGLAALITDGPGGSKWMYGKHAGKVFYDLTGNSRSDTITNSDGMGEKFGVNGSVW 480  
Db 455 GSGLAALITDGPGGSKWMYGKHAGKVFYDLTGNSRSDTITNSDGMGEKFGVNGSVW 514  
  
Qy 481 VPRKTTVSTIARPIITRPWTGFEVFRWTEPRLVAMP 515  
Db 515 VPRKTTVSTIARPIITRPWTGFEVFRWTEPRLVAMP 549  
  
RESULT 11  
ABU03084  
ID ABU03084 standard; protein; 549 AA.  
XX  
AC ABU03084;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Alpha amylase polypeptide #45.  
XX  
KW Alpha amylase; enzyme; starch linkage hydrolysis; starch liquefaction;  
KW starch breakdown catalysis; textile desizing; lignocellulosic fibre;  
KW enzymatic de-inking; recycled paper; high-maltose syrup; dough;  
KW high glucose syrup; corn-wet milling process; detergent; baking process;  
KW beverage; oil field; fuel ethanol; brewing process; staling;  
KW starch modification.  
XX  
OS Unidentified.  
XX  
PN WO200268589-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 21-FEB-2002; 2002WO-US005068.

XX 21-FEB-2001; 2001US-0270495P.  
PR 21-FEB-2001; 2001US-0270496P.  
PR 14-MAY-2001; 2001US-0291122P.  
XX  
PA (DIVE-) DIVERSA CORP.  
XX  
XX Callen W, Richardson T, Frey G;  
XX WPI; 2003-018656/01.  
DR N-PSDB; ABX08455.  
XX  
XX Novel purified polypeptide with alpha-amylase activity, useful e.g. for  
PT liquefying starch, for textile desizing, for treating lignocellulosic  
PT fibers, and for producing high-maltose or high-glucose syrup.  
XX  
XX Claim 30; Fig 16; 30pp; English.  
XX  
CC The invention relates to a purified polypeptide with alpha-amylase  
CC activity and the polynucleotide encoding it. The polypeptide is useful  
CC for hydrolysing starch linkages, for catalysing the breakdown of a  
CC starch, for modifying small molecules, for liquefying starch, for washing  
CC an object, for textile desizing, for treating lignocellulosic fibers, for  
CC improving fibre properties, for enzymatic de-inking of recycled paper  
CC pulp, for producing a high-maltose or high-glucose syrup or a mixed  
CC subterranean formation by removing a viscous, starch-containing, damaging  
CC fluid formed during production operations and found within the  
CC subterranean formation which surrounds a completed well bore. The  
CC polypeptide is also useful for preparing a dough or a baked product  
CC prepared from the dough and in corn-wet milling processes, detergents,  
CC baking processes, beverages, oil fields (fuel ethanol), brewing processes  
CC and starch modification in the paper and pulp industry, for removing  
CC starch containing stains from a material and for reducing staling of  
CC bakery products. Sequences ABU03040-ABU03144 represent alpha amylase  
CC polypeptides of the invention  
XX  
SQ Sequence 549 AA;  
  
Query Match 99.2%; Score 2832; DB 6; Length 549;  
Best Local Similarity 99.4%; Pred. No. 7.5e-244;  
Matches 512; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYY 60  
Db 35 AAPFNGTMQYFEWYLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYY 94  
  
Qy 61 DLYDLGEFNQKGTVRTKYGTAKYQLOAQIAHAAGMOYADVDFHKGADGTWDAVE 120  
Db 95 DLYDLGEFNQKGTVRTKYGTAKYQLOAQIAHAAGMOYADVDFHKGADGTWDAVE 154  
  
Qy 121 VNPSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180  
Db 155 VNPSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 214  
  
Qy 181 IGKAWDWEVDTENGNYDYLWADLMDHPEVVTTELKNWGWYNTTIDGFRDLDAVKHIK 240  
Db 215 IGKAWDWEVDTENGNYDYLWADLMDHPEVVTTELKNWGWYNTTIDGFRDLDAVKHIK 274  
  
Qy 241 FSFPFDWLSVRSQTKPLFTVGEWYSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 300  
Db 275 FSFPFDWLSVRSQTKPLFTVGEWYSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 334  
  
Qy 301 SGGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGALQSWDVPWFKPLAYAFILTRQEG 360  
Db 335 SGGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGALQSWDVPWFKPLAYAFILTRQEG 394  
  
Qy 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 420  
Db 395 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 454  
  
Qy 421 GSGLAALITDGPGGSKWMYGKHAGKVFYDLTGNSRSDTITNSDGMGEKFGVNGSVW 480  
PF |||||



Db	455	GSLAALITDGGSGKMYVQKQHAGKVFYDLTGNRSDTVTINS	DGNGEFGKNGSSVSW	514
Qy	481	VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP	515	
Db	515	VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP	549	
RESULT 12				
AAAP70338				
ID	AAAP70338	standard; protein; 549 AA.		
XX	AAAP70338;			
XX	24-OCT-2003	(revised)		
DT	25-MAR-2003	(revised)		
DT	12-MAR-1991	(first entry)		
XX	Alpha-amylase gene product.			
XX	Bacillus licheniformis.			
XX	Geobacillus stearothermophilus.			
XX	EP208491-A.			
XX	14-JAN-1987.			
XX	30-JUN-1986;	86EP-00305057.		
XX	03-JUL-1985;	85US-00752267.		
PR	(GEMV ) GENENCOR INC.			
XX	Gray GL;			
XX	WPI; 1987-009126/02.			
DR	N-PSDB; AAN70538.			
XX	Hybrid DNA sequence prodn. - by forming a circular vector from 3 DNA			
PT	sequences and transforming a rec positive microorganism with the vector.			
XX	Disclosure; Fig 2; 54pp; English.			
CC	A method is claimed for transforming a host with a recombinant Bacillus			
CC	alpha-amylase gene, made up of a steaothermophilus N-terminal and a			
CC	licheniformis C-terminal. The method involves constructing a plasmid with			
CC	a sequence separating the two terminals containing a unique restriction			
CC	site which may be cut allowing the plasmid to recombine. See also			
CC	AAN70539. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-			
CC	OCT-2003 to standardise OS field)			
XX	Sequence 549 AA;			
Qy	Query Match	98.4%; Score 2808; DB 1; Length 549;		
Db	Best Local Similarity	98.6%; Pred. No. 1e-241;		
XX	Matches 508; Conservative	2; Mismatches 5; Indels 0; Gaps 0;		
Qy	1	AAPNGTMMQYFEWYLPDDGTLTKVANEANNSLGLTALWLPAYKGTSSRSDVG	60	
Db	35	AAPNGTMMQYFEWYLPDDGTLTKVANEANNSLGLTALWLPAYKGTSSRSDVG	94	
Qy	61	LDYDLGFEFNQGTGRTKYGTAQYLOAQIAAAGMOMVADVDFDHKGADGTWDAVE	120	
Db	95	LDYDLGFEFNQGTGRTKYGTAQYLOAQIAAAGMOMVADVDFDHKGADGTWDAVE	154	
Qy	121	VNPSDRNQEISGTQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180	
Db	155	VNPSDRNQEISGTQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	214	
Qy	181	IGKAWDEVDTPENGNDYLMYADLMDHPEVVTTELKNGKGYVNTNIDGFRLLDAVKHIK	240	
Db	215	IGKAWDEVDTPENGNDYLMYADLMDHPEVVTTELKNGKGYVNTNIDGFRLLDAVKHIK	274	
Qy	241	FSFPDMLSVRSQTKPLFTVGEYWSYDINKLHNITKTDGTMSLFADAPLHNKFTYASK	300	
Db	275	FSFPDMLSVRSQTKPLFTVGEYWSYDINKLHNITKTDGTMSLFADAPLHNKFTYASK	334	
Qy	301	SGGAFDMRTLTMTNLTAKDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG	360	
Db	335	SGGAFDMRTLTMTNLTAKDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG	394	
Qy	361	YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP	420	
Db	395	YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP	454	
Qy	421	GSLAALITDGGSGKMYVQKQHAGKVFYDLTGNRSDTVTINS	DGNGEFGKNGSSVSW	480
Db	455	GSLAALITDGGSGKMYVQKQHAGKVFYDLTGNRSDTVTINS	DGNGEFGKNGSSVSW	514
Qy	481	VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP	515	
Db	515	VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP	549	
RESULT 13				
AAW31502				
ID	AAW31502	standard; protein; 515 AA.		
XX	AAW31502;			
XX	08-APR-1998	(first entry)		
DT	Bacillus sp.	alpha amylase.		
DE	Alpha amylase; hard surface cleaning; dishwashing; laundry.			
XX	Bacillus sp.			
OS	WO9732961-A2.			
PN	12-SEP-1997.			
XX	04-MAR-1997;	97WO-US003635.		
XX	07-MAR-1996;	96WO-US003276.		
PR	(PROC ) PROCTER & GAMBLE CO.			
XX	Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;			
PI	Ward G;			
XX	WPI; 1997-457524/42.			
XX	Detergent compositions for hard surface cleaning and laundry use -			
PT	contains Bacillus derived alpha amylase with improved thermostability,			
PT	reduced calcium ion dependency etc.			
XX	Claim 1; Page 91; 97pp; English.			
XX	The present sequence is a Bacillus sp. alpha amylase with a specific			
CC	activity at least 25% higher than that of Termamyl (RTM) at 25 to 55			
CC	degrees C at pH 8 to 10, measured by the Phadebas (RTM) activity test. It			
CC	is of use in hard surface cleaning, hand or machine dishwashing and			
CC	laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain			
CC	removal and fabric care are obtained by using it at a concentration of			
CC	0.00018 to 0.06%			
XX	Sequence 515 AA;			
Qy	Query Match	97.7%; Score 2787; DB 2; Length 515;		
Db	Best Local Similarity	98.1%; Pred. No. 7.2e-240;		
XX	Matches 505; Conservative	2; Mismatches 8; Indels 0; Gaps 0;		
Qy	1	AAPNGTMMQYFEWYLPDDGTLTKVANEANNSLGLTALWLPAYKGTSSRSDVG	60	
Db	1	AAPNGTMMQYFEWYLPDDGTLTKVANEANNSLGLTALWLPAYKGTSSRSDVG	60	

Qy 61 DLYDLGEBFNQKGTVRTKYGTKAQYLQAIQAAHAAGMOYVADVPDHPKGGADGTETWDAVE 120  
 Db 61 DLYDLGEBFNQKGTVRTKYGTKAQYLQAIQAAHAAGMOYVADVPDHPKGGADGTETWDAVE 120  
 Qy 121 VNPDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 Db 121 VNPDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 Qy 181 IGKAWDEVDTEGNYDYLMDADLMDHPEVVTTELKNGKMYVNTTNIIDGFRDLDAVKHIK 240  
 Db 181 IGKAWDEVDTEGNYDYLMDADLMDHPEVVTTELKNGKMYVNTTNIIDGFRDLDAVKHIK 240  
 Qy 241 FSPFPDMLSVRSOTGKPLFTVGYWYSYDINKLHNYITKTGTMSLDFDAPLHNKFTYASK 300  
 Db 241 FSPFPDMLSVRSOTGKPLFTVGYWYSYDINKLHNYITKTGTMSLDFDAPLHNKFTYASK 300  
 Qy 301 SGGAFDMRTLMNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
 Db 301 SGGAFDMRTLMNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
 Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
 Db 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
 Qy 421 GSGLAALITDGPGGSKMYVKGQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480  
 Db 421 GSGLAALITDGPGGSKMYVKGQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480  
 Qy 481 VPRKTTVSTIARPIITRPWTGFEVRWTEPRLVAMP 515  
 Db 481 VPRKTTVSTIARPIITRPWTGFEVRWTEPRLVAMP 515  
 RESULT 14  
 AAW48263  
 ID AAW48263 standard; protein; 515 AA.  
 AC AC  
 XX XX  
 DT 02-JUL-1998 (first entry)  
 DE Bacillus sp. alpha amylase protein #3.  
 KW Alpha amylase; stain digestion; detergent; fabric laundry performance.  
 XX Bacillus sp.  
 XX WO9805748-A1.  
 XX 12-FEB-1998.  
 XX 01-AUG-1996; 96WO-US012612.  
 XX 01-AUG-1996; 96WO-US012612.  
 XX (PROC ) PROCTER & GAMBLE CO.  
 XX Baech AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;  
 XX WPI; 1998-159168/14.  
 XX Use of specific alpha-amylase enzymes - in laundry detergent compositions  
 XX to provide effective cleaning and whitening of dingy fabrics.  
 XX Claim 1; Page 74; 82pp; English.  
 XX This sequence represents an alpha amylase from Bacillus sp. which is used  
 XX in a laundry detergent. The detergent compositions can be used for  
 XX boosting fabric laundry performance or for dingy fabric cleanup  
 XX Sequence 515 AA;

Query Match 97.7%; Score 2787; DB 2; Length 515;  
 Best Local Similarity 98.1%; Pred. No. 7.2e-240;  
 Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANBANNLSSIGITALLWLPAYKGTSRSDVGVY 60  
 Db 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANBANNLSSIGITALLWLPAYKGTSRSDVGVY 60  
 Qy 61 DLYDLGEBFNQKGTVRTKYGTKAQYLQAIQAAHAAGMOYVADVPDHPKGGADGTETWDAVE 120  
 Db 61 DLYDLGEBFNQKGTVRTKYGTKAQYLQAIQAAHAAGMOYVADVPDHPKGGADGTETWDAVE 120  
 Qy 121 VNPDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 Db 121 VNPDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 Qy 181 IGKAWDEVDTEGNYDYLMDADLMDHPEVVTTELKNGKMYVNTTNIIDGFRDLDAVKHIK 240  
 Db 181 IGKAWDEVDTEGNYDYLMDADLMDHPEVVTTELKNGKMYVNTTNIIDGFRDLDAVKHIK 240  
 Qy 241 FSPFPDMLSVRSOTGKPLFTVGYWYSYDINKLHNYITKTGTMSLDFDAPLHNKFTYASK 300  
 Db 241 FSPFPDMLSVRSOTGKPLFTVGYWYSYDINKLHNYITKTGTMSLDFDAPLHNKFTYASK 300  
 Qy 301 SGGAFDMRTLMNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
 Db 301 SGGAFDMRTLMNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
 Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
 Db 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
 Qy 421 GSGLAALITDGPGGSKMYVKGQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480  
 Db 421 GSGLAALITDGPGGSKMYVKGQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480  
 Qy 481 VPRKTTVSTIARPIITRPWTGFEVRWTEPRLVAMP 515  
 Db 481 VPRKTTVSTIARPIITRPWTGFEVRWTEPRLVAMP 515  
 RESULT 15  
 AAY25153  
 ID AAY25153 standard; protein; 515 AA.  
 AC AC  
 XX XX  
 DT 27-AUG-1999 (first entry)  
 DE Bacillus sp. alpha-amylase protein fragment 3.  
 KW Alpha-amylase; cleaning composition; protease variant; spot removal;  
 KW detergent composition; hard surface cleaning; fabric cleaning;  
 KW dishwashing composition; oral cleaning composition; personal cleansing;  
 KW stain removal; soil removal; whiteness maintenance; dingy cleanup;  
 KW film removal.  
 XX Bacillus sp.  
 XX WO9920723-A2.  
 XX 29-APR-1999.  
 XX 23-OCT-1998; 98WO-US022486.  
 XX 23-OCT-1997; 97US-00956323.  
 XX 23-OCT-1997; 97US-00956324.  
 XX 23-OCT-1997; 97US-00956564.  
 XX (PROC ) PROCTER & GAMBLE CO.  
 XX Ghosh CK, Baech AC, Ohtani R, Busch A, Showell MS;

DR WPI; 1999-404706/34.  
XX Cleaning compositions used in e.g. detergent for cleaning hard surfaces  
PT or fabrics, dishwashing or oral cleaning comprises protease and amylase  
PT variants having amino acid residues.  
XX Claim 1b(viii); Page 169; 169pp; English.  
PS  
PS  
XX This invention describes novel cleaning compositions which contain a  
CC protease variant with an amino acid substitution corresponding to  
CC position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant.  
CC The compositions can be used in e.g. detergent compositions, for cleaning  
CC hard surfaces or fabrics, dishwashing compositions, oral cleaning  
CC compositions, detergent cleaning compositions and personal cleansing  
CC compositions. The combination of protease variants and alpha-amylase  
CC variants in cleaning compositions can provide improved and enhanced  
CC cleaning ability, including stain and/or soil removal and/or reduction  
CC and/or whiteness maintenance and/or dingy cleanup and/or spot and/or film  
CC removal and/or reduction, over conventional enzyme-containing cleaning  
CC compositions  
XX  
XX Sequence 515 AA;  
SQ  
Query Match 97.7%; Score 2787; DB 2; Length 515;  
Best Local Similarity 98.1%; Pred. No. 7.2e-240;  
Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 1 AAPFNGTMMQYFWEYLPDDGTLTKVANEANNLSSLGITALLWLPAYKGTSRSDVG YGY 60  
DB 1 AAPFNGTMMQYFWEYLPDDGTLTKVANEANNLSSLGITALLWLPAYKGTSRSDVG YGY 60  
QY 61 DLYDLGEFNGKGVTRTKYKTAQYQLQIAAHAGMQVYADVDPDHKGADGTIEWDVAVE 120  
DB 61 DLYDLGEFNGKGVTRTKYKTAQYQLQIAAHAGMQVYADVDPDHKGADGTIEWDVAVE 120  
QY 121 VNPSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKWYHFDGVDWDESKLSRIYKFRG 180  
DB 121 VNPSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKWYHFDGVDWDESKLSRIYKFRG 180  
QY 181 IGRADWEVDTEGNGYDYLMDYADLDMDHPEVVTTELKNGKMYVNTTIDGFRDLDAVKHIK 240  
DB 181 IGRADWEVDTEGNGYDYLMDYADLDMDHPEVVTTELKNGKMYVNTTIDGFRDLDAVKHIK 240  
QY 241 FSFPFDWLSYVRSQTGKPLFTVGEYSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK 300  
DB 241 FSFPFDWLSYVRSQTGKPLFTVGEYSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK 300  
QY 301 SGGAFTMRTLTMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG 360  
DB 301 SGGAFTMRTLTMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG 360  
QY 361 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARRDYAGTOHDYLDHSDIIGWTREGGTEKP 420  
DB 361 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARRDYAGTOHDYLDHSDIIGWTREGGTEKP 420  
QY 421 GSGLAALITDGPGGSKWYVKQHAGKVFDLTGNRSDTITNSDGMGEFKVNGSGSVW 480  
DB 421 GSGLAALITDGPGGSKWYVKQHAGKVFDLTGNRSDTITNSDGMGEFKVNGSGSVW 480  
QY 481 VPRKTTVSTIARPTITRPTWGEFVRWTEPRLVAMP 515  
DB 481 VPRKTTVSTIARPTITRPTWGEFVRWTEPRLVAMP 515

Search completed: October 7, 2004, 00:12:16  
Job time : 65.1733 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 15.8068 Seconds  
(without alignments)  
3134.012 Million cell updates/sec

Title: US-09-925-576C-6  
Perfect score: 2854  
Sequence: 1 AAPFNGTMMQYFEWYLPDDG.....TRPWTGEFVRWTEPRILVAMP 515  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2854	100.0	549	1 A54541	alpha-amylase (EC
2	2812	98.5	549	1 A24549	alpha-amylase (EC
3	2787	97.7	549	1 A24436	alpha-amylase (EC
4	2727.5	95.6	548	1 ALBSF	alpha-amylase (EC
5	1874.5	65.7	518	1 A27705	alpha-amylase (EC
6	1794.5	62.9	512	1 ALBSL	alpha-amylase (EC
7	1773.5	62.1	514	1 ALBSN	alpha-amylase (EC
8	1345.5	47.1	492	2 AH2079	alpha-amylase (imp
9	1315	46.1	484	2 G95160	alpha-amylase (imp
10	1311	45.9	484	2 F98026	alpha-amylase (EC
11	1278.5	44.8	493	2 S15733	alpha-amylase (EC
12	1229	43.1	491	2 C86781	alpha-amylase (imp
13	1112.5	39.0	494	1 B45738	alpha-amylase (EC
14	1101.5	38.6	494	2 AD0751	cytoplasmic alpha-
15	1078.5	37.8	495	2 AD3038	alpha-amylase (imp
16	1078.5	37.8	506	2 G98247	cytoplasmic alpha-
17	1074.5	37.6	495	1 A45738	alpha-amylase (EC
18	1074.5	37.6	495	2 B90962	cytoplasmic alpha-
19	1055.5	37.0	495	2 B85810	cytoplasmic alpha-
20	354.5	12.4	217	2 AL9506	alpha-amylase (EC
21	326.5	11.4	482	2 S31478	alpha-amylase (EC
22	313	11.0	713	1 ALBSG7	cyclomaltodextrin
23	307	10.8	826	2 E96720	probable alpha-amy
24	307	10.8	1196	2 A29130	beta-amylase (EC 3
25	302.5	10.6	440	2 S14958	alpha-amylase (EC
26	302	10.6	713	2 S09196	cyclomaltodextrin
27	300	10.5	713	2 A58800	cyclomaltodextrin
28	296	10.4	423	2 T09942	alpha-amylase (EC
29	295	10.3	428	2 T05521	alpha-amylase (EC

RESULT 1

A54541  
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI1792)  
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C;Species: Bacillus stearothermophilus  
C;Date: 28-Oct-1994 #sequence\_revision 18-Aug-1995 #text\_change 13-Jun-1997  
C;Accession: A54541  
R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.  
FEMS Microbiol. Lett. 77, 271-276, 1991  
A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.  
A;Reference number: A54541  
A;Accession: A54541  
A;Molecule type: DNA  
A;Residues: 1-549 <TOR>  
A;Cross-references: GB:X59476  
A;Experimental source: chromosomal DNA of strain DNI1792  
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the  
C;Genetics:  
A;Start codon: GTG  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amyliolofaciens type; alpha-amylase core homology  
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac  
F;1-34/Domain: signal sequence #status predicted <SIG>  
F;35-549/Product: alpha-amylase #status predicted <MAT>  
F;235-368/Domain: alpha-amylase core homology <AMY>  
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted  
F;268,298,365/Active site: Asp, Glu, Asp #status predicted  
Query Match 100.0%; Score 2854; DB 1; Length 549;  
Best Local Similarity 100.0%; Pred. No. 2.3e-198; Indels 0; Gaps 0;  
Matches 515; Conservative 0; Mismatches 0;  
Qy 1 AAPFNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALLWLPAYKGTSRSDVG YV 60  
Db 35 AAPFNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALLWLPAYKGTSRSDVG YV 94  
Qy 61 DLVDLGFBNKGVTRTKYTKAQYLOIAQAAHAGMQYADVDFDHKGADGTIEWDAVE 120  
Db 95 DLVDLGFBNKGVTRTKYTKAQYLOIAQAAHAGMQYADVDFDHKGADGTIEWDAVE 154  
Qy 121 VNPEDRNOEISGTYQIOAWTKEDFPGRGNTYSSPKWYHFDGVDWDESKLSRIYKFRG 180  
Db 155 VNPEDRNOEISGTYQIOAWTKEDFPGRGNTYSSPKWYHFDGVDWDESKLSRIYKFRG 214  
Qy 181 IGKAWDEVDTENGNDYLMYADLMDHPEVVTTELKWKQWYVNTTIDGFRDLDAVKHK 240  
Db 215 IGKAWDEVDTENGNDYLMYADLMDHPEVVTTELKWKQWYVNTTIDGFRDLDAVKHK 274  
Qy 241 FSFPFDWLVSYSRSGTKPLFTVGVYSYDINKLHNYITKTDGTWLSLFDAPLHNFYASK 300

ALIGNMENTS

Db 275 FSFPDMLSVRSQTKPLFTVGEYMSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 334  
QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDWPKFPLAYAFILTRQEG 360  
Db 335 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDWPKFPLAYAFILTRQEG 394  
QY 361 YPCVFYGDYGYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYDLHSDIIGWTRGGGTEKP 420  
Db 395 YPCVFYGDYGYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYDLHSDIIGWTRGGGTEKP 454  
QY 421 GSGLAALITDGGGSKMWYVQKHAGKVFYDLTGNRSDTVTINSDDGGEFKVNGGSVSW 480  
Db 455 GSGLAALITDGGGSKMWYVQKHAGKVFYDLTGNRSDTVTINSDDGGEFKVNGGSVSW 514  
QY 481 VPRKTTVSTIARPIITRPTWTEPRVWAMP 515  
Db 515 VPRKTTVSTIARPIITRPTWTEPRVWAMP 549  
RESULT 2  
A24549  
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)  
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C;Species: Bacillus stearothermophilus  
C;Date: 30-Jun-1988 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
C;Accession: A24549; I39501; I39770  
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamaa, M.H.; Kindle, K.L.; Carmona, C.; Requadt,  
J. Bacteriol. 166, 635-643, 1986  
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothe  
A;Reference number: A91817; MUID:86195857; PMID:3009417  
A;Accession: A24549  
A;Molecule type: DNA  
A;Residues: 1-549 <GRA>  
A;Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513  
A;Experimental source: genomic DNA of strain NZ-3  
R;Sachon, H.; Nishida, H.; Isono, K.  
J. Bacteriol. 170, 1034-1040, 1988  
A;Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista  
A;Reference number: I39501; MUID:88139156; PMID:3257753  
A;Accession: I39501  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 536-549 <RES>  
A;Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478  
A;Experimental source: strain DY-5  
A;Accession: I39770  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 536-549 <RE2>  
A;Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486  
A;Experimental source: strain 799  
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the  
C;Genetics:  
A;Start codon: GTG  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology  
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc  
F;1-34/Domain: signal sequence #status predicted <SIG>  
F;35-549/Product: alpha-amylase #status predicted <MAT>  
F;235-368/Domain: alpha-amylase core homology <AMY>  
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted  
F;268,298,365/Active site: Asp, Glu, Asp #status predicted  
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Best Local Similarity 98.8%; Pred. No. 2.5e-195;  
Matches 509; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 AAPFNGTMMQYFEWYLPDDGTLTKVANEANLSSIGITALWLPYPAYKGTSRSDVGYGYY 60  
Db 35 AAPFNGTMMQYFEWYLPDDGTLTKVANEANLSSIGITALWLPYPAYKGTSRSDVGYGYY 94

QY 61 DLYDLGEFNQKGVTRTKYQIAOIAAAGHQVYADVDFVDFHKGAGDGTWDAVE 120  
Db 95 DLYDLGEFNQKGVTRTKYQIAOIAAAGHQVYADVDFVDFHKGAGDGTWDAVE 154  
QY 121 VNPSSDRNQETISGTYQIOAMTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
Db 155 VNPSSDRNQETISGTYQIOAMTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214  
QY 181 IGKAWDEVDVTENGNDYLMYADLDMHDPEVVTTELKNGWKYVNTTNDGFRDLDAVKHIK 240  
Db 215 IGKAWDEVDVTENGNDYLMYADLDMHDPEVVTTELKNGWKYVNTTNDGFRDLDAVKHIK 274  
QY 241 FSFPDMLSVRSQTKPLFTVGEYMSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 300  
Db 275 FSFPDMLSVRSQTKPLFTVGEYMSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 334  
QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDWPKFPLAYAFILTRQEG 360  
Db 335 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDWPKFPLAYAFILTRQEG 394  
QY 361 YPCVFYGDYGYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYDLHSDIIGWTRGGGTEKP 420  
Db 395 YPCVFYGDYGYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYDLHSDIIGWTRGGGTEKP 454  
QY 421 GSGLAALITDGGGSKMWYVQKHAGKVFYDLTGNRSDTVTINSDDGGEFKVNGGSVSW 480  
Db 455 GSGLAALITDGGGSKMWYVQKHAGKVFYDLTGNRSDTVTINSDDGGEFKVNGGSVSW 514  
QY 481 VPRKTTVSTIARPIITRPTWTEPRVWAMP 515  
Db 515 VPRKTTVSTIARPIITRPTWTEPRVWAMP 549  
RESULT 3  
A24436  
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid PAT5  
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C;Species: Bacillus stearothermophilus  
C;Date: 05-Jun-1987 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
C;Accession: A24436; I39777  
R;Nakajima, R.; Imanaka, T.; Aiba, S.  
J. Bacteriol. 163, 401-406, 1985  
A;Reference number: A24436; MUID:85234394; PMID:3924897  
A;Accession: A24436  
A;Molecule type: DNA  
A;Residues: 1-549 <NAK>  
A;Cross-references: GB:M11450  
A;Experimental source: plasmid PAT5  
A;Note: amino end of the mature protein also determined  
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.  
Gene 96, 37-41, 1990  
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con  
A;Reference number: I39772; MUID:91092499; PMID:2265757  
A;Accession: I39777  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-45 <RES>  
A;Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515  
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the  
C;Genetics:  
A;Gene: amys  
A;Genome: plasmid  
A;Start codon: GTG  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology  
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc  
F;1-34/Domain: signal sequence #status predicted <SIG>  
F;35-549/Product: alpha-amylase #status experimental <MAT>  
F;235-368/Domain: alpha-amylase core homology <AMY>  
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted  
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 97.7%; Score 2787; DB 1; Length 549;  
 Best Local Similarity 98.1%; Pred. No. 1.66-193;  
 Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPNGTMMQYFEWYLPDDGTLWTKVANEANNSSLGITLWLPYPAYKGTSRSDVGVGY 60  
 DB 35 AAPNGTMMQYFEWYLPDDGTLWTKVANEANNSSLGITLWLPYPAYKGTSRSDVGVGY 94

QY 61 DLYDLGFEFNQKGTVRTKYGTAKQYLQAIQAAHAGMOMVYADVVDHKGADGTWDAVE 120  
 DB 95 DLYDLGFEFNQKGTVRTKYGTAKQYLQAIQAAHAGMOMVYADVVDHKGADGTWDAVE 154

QY 121 VNPSDRNQEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 DB 155 VNPSDRNQEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214

QY 181 IGKAWDEVDTEGNDYDLMYADLDMDHPEVVTTELKNGKWYVNTTNDGFRDLDAVKHIK 240  
 DB 215 IGKAWDEVDTEGNDYDLMYADLDMDHPEVVTTELKNGKWYVNTTNDGFRDLDAVKHIK 274

QY 241 FSFPDNLVSRSVRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300  
 DB 275 FSFPDNLVSRSVRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 334

QY 301 SGGAFTMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360  
 DB 335 SGGAFTMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 394

QY 361 YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 420  
 DB 395 YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 454

QY 421 GSGLAALITDGPCKGKMMYVKGQKAGKVFYDLTGNSRSDTVTINSDDGGEFKVNGSGSVW 480  
 DB 455 GSGLAALITDGPCKGKMMYVKGQKAGKVFYDLTGNSRSDTVTINSDDGGEFKVNGSGSVW 514

QY 481 VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP 515  
 DB 515 VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP 549

RESULT 4  
 ALBSF  
 N;Alternate names: 1.4-alpha-D-glucan glucohydrolase (strain DY-5) plasmid  
 C;Species: Bacillus stearothermophilus  
 C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 16-Feb-1997  
 C;Accession: A91999; B91999; A91804; A00845  
 R;Ihara, H.; Sasaki, T.; Teubol, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.  
 J. Biochem. 98, 95-103, 1985  
 A;Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology bet  
 A;Reference number: A91999; MUID:86008166; PMID:3876333  
 A;Accession: A91999  
 A;Molecule type: DNA  
 A;Residues: 1-548 <IH1>  
 A;Cross-references: GB:X02769  
 A;Experimental source: plasmid PHI300 from strain DY-5  
 A;Accession: B91999  
 A;Molecule type: protein  
 A;Residues: 35-48 <IH2>  
 A;Experimental source: strain DY-5  
 R;Tsukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,  
 J. Bacteriol. 164, 1182-1187, 1985  
 A;Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-p  
 A;Reference number: A91804; MUID:86059211; PMID:2999073  
 A;Accession: A91804  
 A;Contents: pBAM101  
 A;Molecule type: DNA  
 A;Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>  
 C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the  
 C;Genetics:  
 A;Genome: plasmid

A;Start codon: GTG  
 C;Function:  
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
 A;Pathway: glycogen/starch degradation  
 C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology  
 C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacch  
 F;1-34/Domain: signal sequence #status predicted <SIG>  
 F;35-548/Product: alpha-amylase #status experimental <MAT>  
 F;235-368/Domain: alpha-amylase core homology  
 F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted  
 F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 95.6%; Score 2727.5; DB 1; Length 548;  
 Best Local Similarity 96.7%; Pred. No. 3.1e-189;  
 Matches 498; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 1 AAPNGTMMQYFEWYLPDDGTLWTKVANEANNSSLGITLWLPYPAYKGTSRSDVGVGY 60  
 DB 35 AAPNGTMMQYFEWYLPDDGTLWTKVANEANNSSLGITLWLPYPAYKGTSRSDVGVGY 94

QY 61 DLYDLGFEFNQKGTVRTKYGTAKQYLQAIQAAHAGMOMVYADVVDHKGADGTWDAVE 120  
 DB 95 DLYDLGFEFNQKGTVRTKYGTAKQYLQAIQAAHAGMOMVYADVVDHKGADGTWDAVE 154

QY 121 VNPSDRNQEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
 DB 155 VNPSDRNQEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214

QY 181 IGKAWDEVDTEGNDYDLMYADLDMDHPEVVTTELKNGKWYVNTTNDGFRDLDAVKHIK 240  
 DB 215 IGKAWDEVDTEGNDYDLMYADLDMDHPEVVTTELKNGKWYVNTTNDGFRDLDAVKHIK 274

QY 241 FSFPDNLVSRSVRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300  
 DB 275 FSFPDNLVSRSVRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 334

QY 301 SGGAFTMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360  
 DB 335 SGGAFTMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 393

QY 361 YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 420  
 DB 394 YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 453

QY 421 GSGLAALITDGPCKGKMMYVKGQKAGKVFYDLTGNSRSDTVTINSDDGGEFKVNGSGSVW 480  
 DB 454 GSGLAALITDGPCKGKMMYVKGQKAGKVFYDLTGNSRSDTVTINSDDGGEFKVNGSGSVW 513

QY 481 VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP 515  
 DB 514 VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP 548

RESULT 5  
 A27705  
 N;Alternate names: 1.4-alpha-D-glucan glucohydrolase; G6-amylase  
 C;Species: Bacillus sp.  
 C;Date: 31-Mar-1989 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
 C;Accession: A27705  
 R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.  
 Biochem. Biophys. Res. Commun. 151, 25-31, 1988  
 A;Title: Nucleotide sequence of the maltohexaose-producing amylase gene from an alkaloph  
 A;Reference number: A27705; MUID:88162814; PMID:3258152  
 A;Accession: A27705  
 A;Molecule type: DNA  
 A;Residues: 1-518 <TSU>  
 A;Cross-references: GB:M18862; NID:gl42496; PIDN:AAA22231.1; PID:gl42497  
 A;Experimental source: chromosomal DNA of strain 707  
 A;Note: amino end of mature protein also determined  
 C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.  
 C;Function:  
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amyloglucosidase type; alpha-amylase core homology  
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;34-518/Product: alpha-amylase #status experimental <WAT>  
F;236-369/Domain: alpha-amylase core homology <AMY>  
F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted  
F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 65.7%; Score 1874.5; DB 1; Length 518;  
Best Local Similarity 67.2%; Pred. No. 1.1e-127;  
Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;

QY 5 NGTMMQYFEWYLPDDGTLTWKVAENANSLGITALMPPAYKGRSDVGYGYDLYD 64  
DB 39 NGTMMQYFEWYLPDNGHNHNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGAYDLYD 98

QY 65 LGEFNQKGTVTYKGTAKYQLOAQAAHAQKVYADVDFHKGAGDTEWDAVENPVS 124  
DB 99 LGEFNQKGTVTYKGTAKYQLOAQAAHAQKVYADVDFHKGAGDTEWDAVENPVS 158

QY 125 DRNOBISGTYQIQAATKDFPGRGNTYSSPKRWVYHFDGVDWDESRKL-SRIYKFRGIGK 183  
DB 159 NNEQVTEGYEIAWTRFDFPGRGNTYSSPKRWVYHFDGVDWDESRKL-SRIYKFRGIGK 218

QY 184 AWDNEVDTENGNYDLYMADMDHPPEVVTTELKNGKMYNTTINDGFRDLDAVKHKIFSF 243  
DB 219 AWDNEVDTENGNYDLYMADMDHPPEVVTTELKNGKMYNTTINDGFRDLDAVKHKIFSF 278

QY 244 FPDMLSVRSOTGKPLFTVGYWYSYDINKLHNYITKTGDTMSLFDAPLHNKFTYASKSGG 303  
DB 279 TRDINHVRSGATGKMFVAFEFKNDLGAETLQKTNMNHVSFVDFPLHNYLNASKSGG 338

QY 304 AFDMRTLMTNLMKDQPTLAVTFVDNHDTPGQALQSWDPWPKFLAYAFILTRQEGYPC 363  
DB 339 NYDMENLFGVTQVQHRSHAVTFVDNHDSPQEEALESFVEWFKFLAYALTILREQGYPS 398

QY 364 VFYGDYGIPOYNTPLSKSKIDPLLIARRDYAYQTQHDYLDHSDIIGWTREGGTEKPGSG 423  
DB 399 VFYGDYGIPTGHPVPMRSKIDPLIARQYAYQKQYQKQNDYLDHSDIIGWTREGGTEKPGSG 458

QY 424 LAALITDGPQSGKMYVQKQAGKVFVDLTGNRSDTTVINSQDQWPKFNGSGSVVWV 481  
DB 459 LATIMSDGAGSGKMYVQKQAGKVFVDLTGNRSDTTVINSQDQWPKFNGSGSVVWV 516

RESULT 6  
ALBSL  
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis  
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C;Species: Bacillus licheniformis  
C;Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000  
C;Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844  
R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uchida, S.  
J. Biochem. 98, 1147-1156, 1985  
A;Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.  
A;Reference number: A91997; MUID:86111694; PMID:2418011  
A;Molecule type: DNA  
A;Residues: 1-162, 'R', 164-512 <YUU>  
A;Cross-references: GB:X03236; NID:g939551; PIDN:CAA26981.1; PID:g939552  
A;Experimental source: ATCC 2781D  
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986  
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus  
A;Reference number: A91817; MUID:86135857; PMID:3009417  
A;Accession: B24549  
A;Molecule type: DNA  
A;Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>  
A;Cross-references: GB:M13256; NID:g142510; PIDN:AAA22240.1; PID:g142511  
A;Experimental source: NCIB 8061  
R;Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.

J. Bacteriol. 158, 369-372, 1984  
A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase  
A;Reference number: A91796; MUID:84185455; PMID:6609154  
A;Accession: A91796  
A;Molecule type: DNA  
A;Residues: 1-104 <STE>  
A;Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433  
R;Sibakov, M.; Palva, I.  
Eur. J. Biochem. 145, 567-572, 1984  
A;Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase  
A;Reference number: A21663; MUID:85076654; PMID:6334606  
A;Accession: A21663  
A;Molecule type: DNA  
A;Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 82, 'E'  
A;Experimental source: chromosomal DNA of ATCC 14580  
A;Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 67  
R;Laoide, B.M.; Chambliss, G.H.; McConnell, D.J.  
J. Bacteriol. 171, 2435-2442, 1989  
A;Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent regulation  
A;Reference number: I39773; MUID:89213924; PMID:2540150  
A;Accession: I39774  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-29 <LDO>  
A;Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590  
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.  
Gene 96, 37-41, 1990  
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid construction  
A;Reference number: I39772; MUID:91092499; PMID:2265757  
A;Accession: I39772  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-32, 'I', <JOR>  
A;Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; PID:g142499  
R;Kuhn, H.; Fietzek, P.P.; Lampen, J.O.  
J. Bacteriol. 149, 372-373, 1982  
A;Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison with the sequence of the 5'-terminal amino acid sequence of Bacillus licheniformis alpha-amylase  
A;Reference number: A26151; MUID:82098050; PMID:6172418  
A;Accession: A26151  
A;Molecule type: protein  
A;Residues: 30-37, 'E', 39-41, 'X', 43-47 <KU>  
R;Machius, M.; Wiegand, G.; Huber, R.  
J. Mol. Biol. 246, 545-559, 1995  
A;Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.2 angstroms  
A;Reference number: S53788; MUID:95182462; PMID:7877175  
A;Accession: S53788  
A;Molecule type: protein  
A;Residues: 'D', 220-227 <MAC>  
A;Note: sequence represents amino end of an internal fragment created by a single enzymatic cleavage  
R;Machius, M.; Wiegand, G.; Huber, R.  
submitted to the Brookhaven Protein Data Bank, July 1995  
A;Reference number: A65206; PDB:1BPL  
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210; 222-511  
A;Note: these structural studies suggest 163 is Leu rather than Arg  
R;Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.  
submitted to the Brookhaven Protein Data Bank, October 1996  
A;Reference number: A6860; PDB:1VJS  
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210; 222-511  
C;Genetics:  
A;Gene: amyL  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amyloglucosidase type; alpha-amylase core homology  
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide degradation  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;20-512/Product: alpha-amylase #status experimental  
F;227-360/Domain: alpha-amylase core homology <AMY>  
F;133,229,264/Binding site: calcium (Asn, Asp, His) #status experimental  
F;260,290,357/Active site: Asp, Glu, Asp #status experimental

Query Match 62.9%; Score 1794.5; DB 1; Length 512;  
Best Local Similarity 65.0%; Pred. No. 6.7e-122;



Matches 316; Conservative 68; Mismatches 97; Indels 5; Gaps 2;

Qy 1 AAPFNGTMOYFEWYLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYGVY 60  
 Db 29 AANLNGTLMQYFEWYMPDNGQHWKRLNDAYSALAEHGITAVWIPPAYKGTSDQADVGYAY 88  
 Qy 61 DLYDLGFBNGKGTVRTKYGTGAQYLQAIQAHAAGMOMVYADVDPDHKGADGTWDAVE 120  
 Db 89 DLYDLGFBHQGTVRTKYGTGKEIQSAIKLSHSRDINVGDVWLNHKGADATEDVTAVE 148  
 Qy 121 VNPDRNQEISGTYQIQAWTKFDPFGNGTYSSEFKRWYHFDGVDWDSRKLRIYKPRG 180  
 Db 149 VDPADRNRVISEGLIKAWTHFFPGRGSTYSDFKWHYHFDGTDWDSRKLRIYKQ- 207  
 Qy 181 IGKAWDEVTENGNYDLYMTADLMDHPEVVTTELKNGKQVYNTNIDGRLLDAVKHIK 240  
 Db 208 -GKAWDEVSNGNYDLYMTADIDYDHPDVAABEIKRWGTWYANLQDLQGRLLDAVKHIK 266  
 Qy 241 FSPFPDMLSVRSOTGKPLFTVGEWMSYDINKLHNYITKTDGTSLEPDAPLHNKFTASK 300  
 Db 267 FSPURDWNVHREKTKEMFTVAETWQNDLGALENYLNKTNFNHSVDFVPLHYQFHAAS 326  
 Qy 301 SGGAFTMTLNTLMDKQPTLAVTFVNDHDEPGQALQSWVDWFKPLAYAFILITREG 360  
 Db 327 QGGGYDMKLLNSTVSKHPLKAVTFVNDHDTQGSLESTVQTFWFKPLAYAFILITRESG 386  
 Qy 361 YPCVFYGDYGI---PQYNIPSLSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGT 417  
 Db 387 YPQVFYGDYGTGDSQREIPALKHKIEPIELKARKQAYGAQHDYFDHHDIVGWTREGDS 446  
 Qy 418 EKPSGLAALITDGPCKSKWYVQKQAGKVPYDITGNRSPTVTINSQGWGEFKVNGGSV 477  
 Db 447 SVANSGLAALITDGPCKSKWYVQKQAGKVPYDITGNRSPTVTINSQGWGEFKVNGGSV 506  
 Qy 478 SVMVPR 483  
 Db 507 SIYQVR 512

RESULT 7  
 ALBISN  
 N:Alternate names: 1,4-alpha-D-glucan precursor - Bacillus amyloliquefaciens  
 C:Species: Bacillus amyloliquefaciens  
 C:Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #text\_change 18-Jun-1999  
 C:Accession: A92389; A90307; I39763; A00843  
 R:Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, I.  
 J. Biol. Chem. 258, 1007-1013, 1983  
 A:Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced fr  
 A:Reference number: A92389; MUID:83108808; PMID:6185474  
 A:Contents: PUB110  
 A:Accession: A92389  
 A:Molecule type: DNA  
 A:Residues: 1-514 <TAX>  
 A:Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA221  
 R:Chung, H.S.; Friedberg, F.  
 Biochem. J. 185, 387-395, 1980  
 A:Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase.  
 A:Reference number: A90307; MUID:80241725; PMID:6156671  
 A:Accession: A90307  
 A:Molecule type: protein  
 A:Residues: 32-53; 'I', 55-63; 'L', 65-78; 'D', 80-83; 'S', 85-222 <CHU>  
 R:Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;  
 Gene 15, 43-51, 1981  
 A:Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t  
 A:Reference number: I39756; MUID:82051296; PMID:6170539  
 A:Accession: I39756  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-96 <RES>  
 A:Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298  
 R:Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.  
 Gene 59, 161-170, 1987

A:Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells by its ow  
 A:Reference number: I39763; MUID:88137952; PMID:2830166  
 A:Accession: I39763  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-39 <RES>  
 A:Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431  
 C:Function:  
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
 A:Pathway: glycogen/starch degradation  
 C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
 C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-51/Product: alpha-amylase #status predicted <MP1>  
 F:229-362/Domain: alpha-amylase core homology <AMY>  
 F:133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted  
 F:262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 62.1%; Score 1773.5; DB 1; Length 514;  
 Best Local Similarity 65.4%; Pred. No. 2.2e-120;  
 Matches 316; Conservative 57; Mismatches 105; Indels 5; Gaps 2;

Qy 5 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYGVYDLYD 64  
 Db 33 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITLWLPAYKGTSRSDVGYGVYDLYD 92  
 Qy 65 LGFEFNQKGTVRTKYGTGAQYLQAIQAHAAGMOMVYADVDPDHKGADGTWDAVEVNPS 124  
 Db 93 LGFEFNQKGTVRTKYGTGAQYLQAIQAHAAGMOMVYADVDPDHKGADGTWDAVEVNPS 152  
 Qy 125 DRNQEISGTYQIQAWTKFDPFGNGTYSSEFKRWYHFDGVDWDSRKLRIYKPRGIGKA 184  
 Db 153 DRNQEISGTYQIQAWTKFDPFGNGTYSSEFKRWYHFDGVDWDSRKLRIYKPRGIGKA 212  
 Qy 185 WDWEVDTEGNYDLYMTADLMDHPEVVTTELKNGKQVYNTNIDGRLLDAVKHIKPSFF 244  
 Db 213 WDWEVDTEGNYDLYMTADLMDHPEVVTTELKNGKQVYNTNIDGRLLDAVKHIKPSFF 272  
 Qy 245 PDWLSYVRSOTGKPLFTVGEWMSYDINKLHNYITKTDGTSLEPDAPLHNKFTASKSGGA 304  
 Db 273 PDWLSYVRSOTGKPLFTVGEWMSYDINKLHNYITKTDGTSLEPDAPLHNKFTASKSGGA 332  
 Qy 305 FDMRTMTNLMKQPTLAVTFVNDHDEPGQALQSWVDWFKPLAYAFILITREGYPCV 364  
 Db 333 FDMRTMTNLMKQPTLAVTFVNDHDEPGQALQSWVDWFKPLAYAFILITREGYPCV 392  
 Qy 365 FYGDYGI---PQYNIPSLSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
 Db 393 FYGDYGI---PQYNIPSLSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 451  
 Qy 421 GSGLAALITDGPCKSKWYVQKQAGKVPYDITGNRSPTVTINSQGWGEFKVNGGSVSW 480  
 Db 452 GSGLAALITDGPCKSKWYVQKQAGKVPYDITGNRSPTVTINSQGWGEFKVNGGSVSW 511  
 Qy 481 VPR 483  
 Db 512 VQK 514

RESULT 8  
 AH2079  
 alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C:Accession: AH2079  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Saemoto, S.; Watanabe, A.; Iriguchi,  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AH2079  
 A:Status: preliminary



Db 63 LGEFNOKGTVRTKGYKEDYLOAIQALKAQGIOPMADVILNHHKAAADHREAFQVIEVDPV 122  
Qy 125 DRNQEISGTYQIQAWTKFDPFGRNTYSSPKRWYHFDGVDWDSRKLRIYKFRGIGKA 184  
Db 123 DRIVELGEPFTINGTSFTDGRQDTYNGFHHWHYHFTGYDADAKRSKSYLILQDNGK 182  
Qy 185 WDWE--VDTEGNYDYLMYADLMDHDEVTTELKNWGWKWTNTNIDGFRDLDAVGHKFS 242  
Db 183 WANEELVDNENGNYYLMDLDPKPEVIQNIYDMADWFMETTVGAGFRDLDAVGHKIDSF 242  
Qy 243 FPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHKNKFTASKSG 302  
Db 243 FMRNFIDMKYKGGDDYFVGEFNSKDEANLDYLEKTEBEHFDLVRLHQNLFASQAG 302  
Qy 303 GAFDMRLTMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEGYP 362  
Db 303 ANYDLRGIFTDSLVELKPDKAVTFVDNHDTRQGALESFVEWPKPAAYALILLRQDGLP 362  
Qy 363 CVFVGYDYGIP-QYNIPSLKSKIDPLLIARDYAYGTHQHYLDHSDIIGWTRREGTEKPG 421  
Db 363 CVFVGYDYGISGQYAOQDFKXILDLRLAIRKDLAYGEGNDYFDHANGIGWVRSAGENQ-- 420  
Qy 422 SGLAALITDGGSKWYVQKQAGKVFYDLTGNRSDTVTINSOGWGEKFGKNGSVSVWV 481  
Db 421 SPIAVLISNDQENSKSMFVGOEWNTQTFVDLLGSHQGVITDEEGYCGFPVARSARSVW- 479  
Qy 482 PRKTTVSTI 490  
Db 480 ---AVNTI 484

RESULT 11  
S15713  
alpha-amylase (EC 3.2.1.1) - Bacillus circulans  
C;Species: Bacillus circulans  
C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 22-Jun-1999  
C;Accession: S15713  
submitted to the EMBL Data Library, May 1991  
A;Reference number: S15713  
A;Accession: S15713  
A;Molecule type: DNA  
A;Residues: 1-493 <MAR>  
A;Cross-references: EMBL:X60779; NID:G39411; PIDN:CAA43194.1; PID:G39412  
C;Genetics:  
A;Gene: amyE  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
P;200-333/Domain: alpha-amylase core homology <AMY>

Query Match 44.8%; Score 1278.5; DB 2; Length 493;  
Best Local Similarity 48.5%; Pred. No. 1.2e-84;  
Matches 232; Conservative 84; Mismatches 159; Indels 3; Gaps 2;

Qy 5 NGTMQYFEWYLPDDGTLWTKVANEANLSSIGITALMLPPAYKGTSSDVGYGVDLYD 64  
Db 4 NHTMQYFEWLAADGDHMKELAEMAPELKAGDITVWVPVTKAVSAEDTGYGYVDLYD 63  
Qy 65 LGEFNOKGTVRTKGYKQYLOAIQAAHAAGQVYADVVDHKGADGTEWDAVEVNP 124  
Db 64 LGEFDQKGTIVTKGYTKQELTEAECQKNGIANTVDLVMHKGADETEYFVIEVDPN 123  
Qy 125 DRNQEISGTYQIQAWTKFDPFGRNTYSSPKRWYHFDGVDWDSRKLRIYKFRGIGKA 184  
Db 124 DRTKEISPEFIEGWTETFTFGRGDQYSSFKWSEHFGTDFDAREERTGVFRIAGENKK 183  
Qy 185 WDWEVDTEGNYDYLMYADLMDHDEVTTELKNWGWKWTNTNIDGFRDLDAVGHKFSFF 244  
Db 184 WNEVNDDEFGNYDLMFANIYNPDVVRREIMDWGKWLIDTLQCGGFRDLDAVGHKIDSF 243

Qy 245 PDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHKNKFTASKSGGA 304  
Db 244 KEFAAEMIRKRGQDFYIVGEFNSNLDACKREFLDYTDYQIDLEFVLSHYKLHEASLGRD 303  
Qy 305 FDMRTLTMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEGYPCV 364  
Db 304 FDLKSKFPDDLTVGTHPHTAVTFVDNHDSDQHEALESWIGDWKFPESAYALTLLRDGYPV 363  
Qy 365 FYGDIYGI--PQYNIPSLKSKIDPLLIARDYAYGTHQHYLDHSDIIGWTRREGTEKPGS 422  
Db 364 FYGDIYGI--PVDKKEILDILLASRCKAYGQEDYFDHANTIGWVRRGVETEGS 422  
Qy 423 GLAALITDGGSKWYVQKQAGKVFYDLTGNRSDTVTINSOGWGEKFGKNGSVSVW 480  
Db 423 GCAVWISNGDDGKRMFIGEHRAGEVWVDLTKSCDDQITIEEDGWATFHVCGGGSVW 480

RESULT 12  
C86781  
alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C;Accession: C86781  
C;Bolooin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s.s.  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: C86781  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-491 <STO>  
A;Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: amyL  
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 43.1%; Score 1229; DB 2; Length 491;  
Best Local Similarity 47.5%; Pred. No. 4.3e-81;  
Matches 231; Conservative 73; Mismatches 176; Indels 6; Gaps 5;

Qy 7 TMQYFEWYLPDDGTLWTKVANEANLSSIGITALMLPPAYKGTSSDVGYGVDLYD 65  
Db 3 TILQAFEWYLPDSQHNWNNIKENIPDLKGLFSGMLPPASKAASGVEDYGYGYDLD 62  
Qy 66 GEFNOKGTVRTKGYKQYLOAIQAAHAAGQVYADVVDHKGADGTEWDAVEVNP 125  
Db 63 GEFNOKGTVRTKGYKQYLOAIQAAHAAGQVYADVVDHKGADGTEWDAVEVNP 121  
Qy 126 RN-QEISGTYQIQAWTKFDPFGRNTYSSPKRWYHFDGVDWDSRKLRIYKFRGIGKA 184  
Db 122 NHLNHNENNTVETVTKFTFPGKQYDNYITWHTNFTGIDYDERKQKEILEFE--GHE 179  
Qy 185 WDWEVDTEGNYDYLMYADLMDHDEVTTELKNWGWKWTNTNIDGFRDLDAVGHKFSFF 244  
Db 180 WNEVNDSENNFDYLMGADLDFSVSETVEQLEKWHWFSEMTKIDGFRDLDAVGHKIDSF 239  
Qy 245 PDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHKNKFTASKSGGA 304  
Db 240 DKWLEQRAKQDLKFLVGETWSDDLKLEYLEYQSSDRQLFVDPVLPFHMKESSTNGE 299  
Qy 305 FDMRTLTMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEGYPCV 364  
Db 300 FDMRTLTMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEGYPCV 359  
Qy 365 FYGDIYGI--PQYNIPSLKSKIDPLLIARDYAYGTHQHYLDHSDIIGWTRREGTEKPGSGL 424  
Db 360 FWGLDYGTPSHVNPVGDNLRTMLAKRDSFELRENDYFDHPDILIGTNTLILKIDNKEYGL 419  
Qy 425 AALITDGGSKWYVQKQAGKVFYDLTGNRSDTVTINSOGWGEKFGKNGSVSVWVPRK 484  
Db 420 SCILTNKNGSKYMIIDKAYAGKVIIDLPGRHEIPTLDQNGGAFFVNDGGSVWVD-K 478

QY 485 TTVSTI 490  
Db 479 EIVSKI 484

## RESULT 13

B45738  
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Salmonella typhimurium

C/Date: 07-Apr-1994 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999

C/Accession: B45738

R/Raba, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R. M.

J. Bacteriol. 174, 6644-6652, 1992

A/Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.

A/Reference number: A45738; MUID:93015717; PMID:1400215

A/Accession: B45738

A/Molecule type: DNA

A/Residues: 1-494 <RAH>

A/Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045

C/Genetics:

A/Gene: amyA

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

C/Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation

F/202-335/Domain: alpha-amylase core homology <AMY>

F/239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.0%; Score 1112.5; DB 1; Length 494;  
Best Local Similarity 44.0%; Pred. No. 1.1e-72;  
Matches 216; Conservative 83; Mismatches 175; Indels 17; Gaps 5;

QY 5 NGTMMQYFEWYLPDDGTLWTKVANEANNLSLIGITALWLPAYKGTSSR-DVGVGVYDLY 63

Db 3 NPTLLQYFHWYYPDGGKLSLAERADGLNDGINWVWLPACKGASGVSGYDYDLF 62

QY 64 DLGEFNQKGTVRTKYGTAKYQYLAQIAHAAGMOYADVVDVFDHKGADGTWDAVEVNP 123

Db 63 DLGEFDQKGTATKYGDKRQLLTALDALKKNIAVLDDVVNHKMGADKERIRVQRVNO 122

QY 124 SDRNQEISGYTQIAWTKFPDPPGRGNTYSSFKRWVHFDDVDWDSRKLSTRYKPRG-I 181

Db 123 DRTQIDDDNIIECEGWTRYTFPARAGQYSNFIWDYHCFSGIDHIEPNDEGDFIKVINDYT 182

QY 182 GKAWDEVDTEGNYDYLMTADLMDHPEVVTTELKNWGWYVNTNIDGPRLDVAKHKF 241

Db 183 GDGWNQVDDEMGNFYLMGENIDFRNHAVTIEIKYWARVWMEQTHCDGFRLDVAKHIA 242

QY 242 SFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDPALHNKFTYASKS 301

Db 243 WFKYEWIEHVQAVAPKPLFVAEYWSHVEDKLQTYIDQVDGKTMFLDAPLOMKFHEASRQ 302

QY 302 GGAFDMRTLMTLMKQDPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEGY 361

Db 303 GAEDYMRHIFTGLVEADPFHATVILVANHDTPQLQALEAPVEPWFKPLAYALILLRENGV 362

QY 362 PCVFYGDYGYIP-----QYNIPSLKSIDPLLIARRDYAYGTOHDYLDHSDIIG 410

Db 363 PSVFYPDLYGASVSDSGENGETCRVDMPIV-NQLDRLLILARQFAHGIQTLFFDHPNCIA 421

QY 411 WTRGGTEKPGSGLAALITDGGGSKMWYVGKHAGKVFDLTGNRSRDTVTINSQGWGEF 470

Db 422 FSRSGTEENP--GCVVVLSNGDDGKTLILGDNVANKTWDRDFSGNRDEYVVTNDQGEATF 479

QY 471 KVNKGGSVSVWV 481

Db 480 FCNAGSVSVWV 490

## RESULT 14

AD0751

cytoplasmic alpha-amylase [imported] - Salmonella enterica subsp. enterica serovar Typhi  
C/Species: Salmonella enterica subsp. enterica serovar Typhi  
A/Note: this species has also been called Salmonella typhi  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AD0751  
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar  
A/Reference number: AB0502; MUID:21534947; PMID:11677608  
A/Accession: AD0751  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-494 <PAR>  
A/Cross-references: GB:AL513382; PIDN:CAD05711.1; PID:g16503204; GSPDB:GN00176  
C/Genetics:  
A/Gene: STY2171  
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 38.6%; Score 1101.5; DB 2; Length 494;  
Best Local Similarity 44.0%; Pred. No. 7e-72;  
Matches 216; Conservative 82; Mismatches 176; Indels 17; Gaps 5;

QY 5 NGTMMQYFEWYLPDDGTLWTKVANEANNLSLIGITALWLPAYKGTSSR-DVGVGVYDLY 63

Db 3 NPTLLQYFHWYYPDGGKLSLAERADGLNDGINWVWLPACKGASGVSGYDYDLF 62

QY 64 DLGEFNQKGTVRTKYGTAKYQYLAQIAHAAGMOYADVVDVFDHKGADGTWDAVEVNP 123

Db 63 DLGEFDQKGTATKYGDKRQLLTALDALKKNIAVLDDVVNHKMGADKERIRVQRVNO 122

QY 124 SDRNQEISGYTQIAWTKFPDPPGRGNTYSSFKRWVHFDDVDWDSRKLSTRYKPRG-I 181

Db 123 DRTQIDDDNIIECEGWTRYTFPARAGQYSNFIWDYHCFSGIDHIEPNDEGDFIKVINDYT 182

QY 182 GKAWDEVDTEGNYDYLMTADLMDHPEVVTTELKNWGWYVNTNIDGPRLDVAKHKF 241

Db 183 GDGWNQVDDEMGNFYLMGENIDFRNHAVTIEIKYWARVWMEQTHCDGFRLDVAKHIA 242

QY 242 SFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDPALHNKFTYASKS 301

Db 243 WFKYEWIEHVQAVAPKPLFVAEYWSHVEDKLQTYIDQADGKTMFLDAPLOMKFHEASRQ 302

QY 302 GGAFDMRTLMTLMKQDPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEGY 361

Db 303 GAEDYMRHIFTGLVEADPFHATVILVANHDTPQLQALEAPVEPWFKPLAYALILLRENGV 362

QY 362 PCVFYGDYGYIP-----QYNIPSLKSIDPLLIARRDYAYGTOHDYLDHSDIIG 410

Db 363 PSVFYPDLYGASVSDSGENGETCRVDMPIV-NQLDRLLILARQFAHGIQTLFFDHPNCIA 421

QY 411 WTRGGTEKPGSGLAALITDGGGSKMWYVGKHAGKVFDLTGNRSRDTVTINSQGWGEF 470

Db 422 FSRSGTEENP--GCVVVLSNGDDGKTLILGDNVANKTWDRDFLGNRSEHVVTNDQGEATF 479

QY 471 KVNKGGSVSVWV 481

Db 480 FCNAGSVSVWV 490

## RESULT 15

AD3038

alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002

C/Accession: AD3038

R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan,  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 9.03245 Seconds  
(without alignments)  
2968.867 Million cell updates/sec

Title: US-09-925-576C-6  
Perfect score: 2854  
Sequence: 1 AAFPNGTMMQYFEWYLPDDG.....TRPWTGEFVRWTSPLVAMP 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2787	97.7	549	1 AMY_BACST	P06279 bacillus sp
2	1874.5	65.7	518	1 AMT6_BACS7	P19571 bacillus sp
3	1797.5	63.0	512	1 AMY_BACLI	P06278 bacillus li
4	1773.5	62.1	514	1 AMY_BACAM	P00692 bacillus am
5	1110.5	38.9	494	1 AMY2_SALTY	P26613 salmonella
6	1074.5	37.6	495	1 AMY2_ECOLI	P26612 escherichia
7	313	11.0	713	1 CDGT_BACSP	P30921 bacillus sp
8	307	10.8	1196	1 AMYB_PAEPO	P21543 paenibacill
9	302.5	10.6	440	1 AM3A_ORYSA	P27932 oryza sativ
10	302	10.6	713	1 CDGT_BACS8	P17692 bacillus sp
11	300	10.5	713	1 CDGT_BACCI	P43379 bacillus ci
12	286.5	10.0	712	1 CDGT_BACS3	P09121 bacillus sp
13	286	10.0	718	1 CDGT_BACLI	P14014 bacillus li
14	284.5	10.0	713	1 CDGT_BACS0	P05618 bacillus sp
15	283	9.9	421	1 AMYA_VIGMU	P17859 vigna mungo
16	282	9.9	718	1 CDGT_BACSS	P31747 bacillus sp
17	280	9.8	413	1 AMY3_WHEAT	P08117 triticum ae
18	278	9.7	718	1 CDGT_BACCI	P30920 bacillus ae
19	275.5	9.7	564	1 AMY4_SCHPO	Q9Y789 schizosacch
20	274.5	9.6	438	1 AM3B_ORYSA	P27937 oryza sativ
21	274.5	9.6	528	1 AMY_BACCI	P08137 bacillus ci
22	273	9.6	710	1 CDGT_THETU	P26827 thermoanaer
23	272.5	9.5	428	1 AMY1_ORYSA	P17654 oryza sativ
24	271.5	9.5	437	1 AM3C_ORYSA	P27939 oryza sativ
25	268.5	9.4	438	1 AMY1_HORVU	P00693 hordeum vul
26	268	9.4	711	1 CDGT_BACST	P31797 bacillus st
27	266.5	9.3	429	1 AMY6_HORVU	P04750 hordeum vul
28	266	9.3	435	1 AM3D_ORYSA	P27933 oryza sativ
29	262.5	9.2	427	1 AMY2_HORVU	P04063 hordeum vul
30	262	9.2	703	1 CDGT_BACS2	P1746 bacillus sp
31	258.5	9.1	368	1 AMY3_HORVU	P04747 hordeum vul
32	257.5	9.0	437	1 AM3E_ORYSA	P27934 oryza sativ
33	253.5	8.9	494	1 AMY1_SACFI	P21567 saccharomyc

RESULT 1

AMY_BACST	AMY_BACST	STANDARD;	PRT;	549 AA.
ID	AC	P06279; Q45519;		
DT	01-JAN-1988	(Rel. 06, Created)		
DT	01-FEB-1996	(Rel. 33, Last sequence update)		
DT	15-MAR-2004	(Rel. 43, Last annotation update)		
DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).			
DE	Glucanohydrolase).			
GN	AMYS.			
OS	Bacillus stearothermophilus.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.			
OX	NCBI_TaxID=1422;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.			
RX	MEDLINE=85234394; PubMed=3924897;			
RA	Nakajima R., Imanaka T., Aiba S.;			
RT	"Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase gene.";			
RL	J. Bacteriol. 163:401-406(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	STRAIN=DV5/PHI300;			
RX	MEDLINE=86008166; PubMed=3876333;			
RA	Ihara H., Sasaki T., Tsuoi A., Yamagata H., Tsukagoshi N., Uda S.;			
RT	"Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology between prokaryotic and eukaryotic alpha-amylases at the active sites.";			
RL	J. Biochem. 98:95-103(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NZ-3;			
RX	MEDLINE=86195857; PubMed=3009417;			
RA	Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L., Carmona C., Requaadt C.;			
RT	"Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus and Bacillus licheniformis.";			
RL	J. Bacteriol. 166:635-643(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Suominen I., Karp M., Lautamo J., Knowles J., Mantsaelae P.;			
RT	"Thermotable alpha amylase of Bacillus stearothermophilus: cloning, expression, and secretion by Escherichia coli.";			
RL	(In) Chaloupka J., Krumphanz V. (eds.); Extracellular enzymes of microorganisms, pp.129-137, Plenum Press, New York (1987).			
RN	[5]			
RP	SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.			
RC	STRAIN=DY-5;			
RX	MEDLINE=86059211; PubMed=2999073;			
RA	Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H., Idota Y., Yamagata H., Uda S.;			
RT	"Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-producing bacillus brevis 47 carrying the Bacillus stearothermophilus amylase gene.";			
RL	J. Bacteriol. 164:1182-1187(1985).			

ALIGNMENTS

34	249	8.7	443	1	AM2A_ORYSA	P27935 oryza sativ
35	248	8.7	498	1	AMYA_ASPAW	Q02905 aspergillus
36	248	8.7	499	1	AMYB_ASPAW	Q02906 aspergillus
37	247	8.7	499	1	AMY_ASPSH	P30292 aspergillus
38	245	8.6	499	1	AMYA_ASPOR	P10529 aspergillus
39	244	8.5	919	1	AMY_STRLI	Q05884 streptomyce
40	242	8.5	445	1	AMC3_ORYSA	P27941 oryza sativ
41	238.5	8.4	498	1	AMY3_DICTH	P14899 dictyoglomu
42	236	8.1	581	1	AMY1_SCHPO	Q09840 schizosacch
43	230.5	8.1	713	1	CDG2_PAEPA	P31835 paenibacill
44	224.5	7.9	704	1	CDGT_BACOH	P27036 bacillus oh
45	224	7.8	624	1	AMY1_LIPKO	Q01117 lipomyces k

[6]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=21125602; PubMed=11226887;  
 RA Suvd D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;  
 RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:  
 RL J. Biochem. 129:461-468 (2001).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
 CC linkages in oligosaccharides and polysaccharides.  
 CC -!- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; M11450; AAA22235.2; -;  
 DR EMBL; X02769; CRA26547.1; -;  
 DR EMBL; M57457; AAA22227.1; -;  
 DR EMBL; M13255; AAA22241.1; -;  
 DR PIR; A24436; A24436.  
 DR PIR; A91999; ALBSF.  
 DR PDB; 1HVX; 05-AUG-03.  
 DR InterPro; IPR006589; Alp amyl cat sub.  
 DR InterPro; IPR006047; Alpha amyl cat.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR SMART; SM00642; Amy; 1.  
 DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
 KW Signal; 3D-structure.  
 FT SIGNAL 1 34  
 FT CHAIN 35 549  
 FT ACT SITE 268 268  
 FT ACT SITE 272 272  
 FT ACT SITE 365 365  
 FT METAL 139 139  
 FT METAL 196 196  
 FT METAL 218 218  
 FT METAL 220 220  
 FT METAL 231 231  
 FT METAL 237 237  
 FT METAL 238 238  
 FT METAL 239 239  
 FT METAL 272 272  
 FT METAL 337 337  
 FT METAL 339 339  
 FT METAL 440 440  
 FT METAL 441 441  
 FT METAL 464 464  
 FT CONFLICT 13 13  
 FT CONFLICT 19 19  
 FT CONFLICT 23 23  
 FT CONFLICT 31 31  
 FT CONFLICT 107 107  
 FT CONFLICT 167 167  
 FT CONFLICT 179 179  
 FT CONFLICT 251 251  
 FT CONFLICT 260 262  
 FT CONFLICT 284 284  
 FT CONFLICT 312 312  
 FT CONFLICT 338 338  
 FT CONFLICT 342 342  
 FT CONFLICT 346 346  
 FT CONFLICT 376 376  
 FT CONFLICT 526 527  
 FT CONFLICT 527 527  
 FT CONFLICT 535 535  
 FT L -> W (IN REF. 3).  
 FT L -> S (IN REF. 3).  
 FT P -> H (IN REF. 2 AND 3).  
 FT A -> T (IN REF. 2 AND 3).  
 FT T -> I (IN REF. 4).  
 FT P -> N (IN REF. 3).  
 FT S -> N (IN REF. 2, 3 AND 4).  
 FT TNI -> RTL (IN REF. 4).  
 FT D -> Y (IN REF. 2, 3 AND 4).  
 FT M -> T (IN REF. 2 AND 3).  
 FT T -> A (IN REF. 2 AND 3).  
 FT R -> S (IN REF. 3).  
 FT T -> N (IN REF. 3).  
 FT WS -> RP (IN REF. 2).  
 FT S -> P (IN REF. 2).  
 FT D -> G (IN REF. 2 AND 3).

SQ SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;  
 Query Match 97.7%; Score 2787; DB 1; Length 549;  
 Best Local Similarity 98.1%; Pred. No. 1.1e-190;  
 Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 AAFENGTMQYFEWYLPDDGTLTKVANEANNLSLIGITLWLPYKGTSGSDVGVY 60  
 DB 35 AAFENGTMQYFEWYLPDDGTLTKVANEANNLSLIGITLWLPYKGTSGSDVGVY 94  
 QY 61 DLYDLGEFNGKGVRTKYGTQKQYLOAIQAHAAGMQVYADVDFHKGADGTEWDAVE 120  
 DB 95 DLYDLGEFNGKGVRTKYGTQKQYLOAIQAHAAGMQVYADVDFHKGADGTEWDAVE 154  
 QY 121 VNPSDRNQETSGYQIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180  
 DB 155 VNPSDRNQETSGYQIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 214  
 QY 181 IGKADWEVDTEGNYDYLMYADLMDHPEVVTLEKNWGWYVNTNIDGFRDLDAVKHIK 240  
 DB 215 IGKADWEVDTEGNYDYLMYADLMDHPEVVTLEKNWGWYVNTNIDGFRDLDAVKHIK 274  
 QY 241 FSPFPDWLSYVRSQTKPLFTVGEVWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300  
 DB 275 FSPFPDWLSYVRSQTKPLFTVGEVWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 334  
 QY 301 SGGADMRMTLMTNLKQOPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQSG 360  
 DB 335 SGGTFDMRTLMTNLKQOPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQSG 394  
 QY 361 YPCVFYGYGIPQYNIPLSKSIDPLLIARDYAYGTQHDYLDHSDIIGTWREGTEKP 420  
 DB 395 YPCVFYGYGIPQYNIPLSKSIDPLLIARDYAYGTQHDYLDHSDIIGTWREGTEKP 454  
 QY 421 GSGLAALITDGGGSKMWYVGHQAGKVPYDITGNRSQDTVTINSQGWGFEKVGSGSVW 480  
 DB 455 GSGLAALITDGGGSKMWYVGHQAGKVPYDITGNRSQDTVTINSQGWGFEKVGSGSVW 514  
 QY 481 VPRKTTVSTIARPIITRPWTGFEVWTEPRVAVWP 515  
 DB 515 VPRKTTVSTIARPIITRPWTGFEVWTEPRVAVWP 549

RESULT 2  
 AMT6\_BACS7 STANDARD; PRT; 518 AA.  
 ID AMT6\_BACS7  
 AC P19571;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amylase)  
 DE (Maltohexao-se-producing amylase) (Exo-maltohexahydrolase).  
 OS Bacillus sp. (strain 707)  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 ON NCBI\_TaxID=1416;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.  
 RX MEDLINE=88162814; PubMed=3258152;  
 RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;  
 RT "Nucleotide sequence of the maltohexao-se-producing amylase gene from  
 RT an alkalophilic Bacillus sp. #707 and structural similarity to  
 RT Biochem. Biophys. Res. Commun. 151:25-31(1988).  
 RL Biochem. Biophys. Res. Commun. 151:25-31(1988).  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages  
 CC in amylaceous polysaccharides so as to remove successive  
 CC maltohexao-se residues from the non-reducing chain ends.  
 CC -!- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By  
 CC similarity).  
 CC -!- PATHWAY: Starch degradation.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
 CC  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
 CC -----  
 DR EMBL; M18862; AAA22231.1; -;  
 DR PIR; A27705; A27705.  
 DR HSP; P06278; 1VJS.  
 DR InterPro; IPR006589; Alp amyl cat sub.  
 DR InterPro; IPR006047; Alpha amyl cat.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR SMART; SM00642; Amy; 1.  
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.  
 FT SIGNAL 1 33  
 FT CHAIN 34 518 GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.  
 FT ACT\_SITE 269 269 BY SIMILARITY.  
 FT ACT\_SITE 273 273 BY SIMILARITY.  
 FT ACT\_SITE 366 366 BY SIMILARITY.  
 FT METAL 139 139 CALCIUM 1 (BY SIMILARITY).  
 FT METAL 196 196 CALCIUM 2 AND SODIUM (BY SIMILARITY).  
 FT METAL 219 219 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY  
 FT SIMILARITY).  
 FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).  
 FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).  
 FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).  
 FT METAL 240 240 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 242 242 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;  
 Query Match 65.78; Score 1874.5; DB 1; Length 518;  
 Best Local Similarity 67.28; Pred. No. 6.8e-126;  
 Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;  
 QY 5 NGTMQVFEWYLPDGLTWTQVANEANLSSLGITLWLPAYKGRSDVGVGYDLYD 64  
 DB 39 NGTMQVFEWYLPDGNHWRNLSDANLSKGITAVIPPAWKAQNDVGVGYDLYD 98  
 QY 65 LGFENQKGTVRTKYGTQALQALQAAHAAQMVYADVFDHKGAGDTEWDAVEVNP 124  
 DB 99 LGFENQKGTVRTKYGTSLQQAQVTSKNGIQVYGVDMHKGADATEMVAEVPN 158  
 QY 125 DRNQEISGTQIQAWTKDFPGRGNTYSSFKRWYHFDGVWDERSKL-SRIYKFRIGK 183  
 DB 159 NRNQEVGTGYTAEWTRDFPGRGNTSSFKRWYHFDGVWDQSRRLNNRIYKFRGHK 218  
 QY 184 AWDWEVDTEGNYDYLMDMDHPVETLKWGKYVNTTNDGFRDLDAVKHIFSP 243  
 DB 219 AWDWEVDTEGNYDYLMDADLMDHPVETLKWGKYVNTTNDGFRDLDAVKHIFSP 278  
 QY 244 FPDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMFLSDAPLHNKFFYTSKSG 303  
 DB 279 TRDWINHVSATGKNMFAVEFWKNDLGAENYLNKTNHNSVDFVPLHYNLYNASKSG 338  
 QY 304 AFDMRTLTMTLMDQPTLATVFDVNDHDEPGQALQSDVDPWFKPLAYAFILTRQEGYPC 363  
 DB 339 NYDMRNTFNGTVQRHPHSHAVTFVDNHDSPQEALESFVEWFKPLAYALTLTREQGYPS 398  
 QY 364 VFYGDYGIPOYNTPSLKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGYKPGSG 423  
 DB 399 VFYGDYGIPOYNTPSLKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGYKPGSG 458  
 QY 424 LAALITDPGGSKMVYGVKQHAGVFYDITGNRSDTITNSDGNFQVNGSVVW 481  
 DB 459 LATIMSDGAGSKMVFGRNKAQGWSDITGNRTGTTINADGNFVNGSVVSIW 516

RESULT 3

AMY\_BACLI STANDARD; PRT; 512 AA.  
 AC P06278; Q84171;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan  
 DE Glucanohydrolase) (BLA).  
 GN AMYS OR AMYL.  
 OS Bacillus licheniformis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1402;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 27811;  
 RX MEDLINE=86111694; PubMed=2418011;  
 RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,  
 RA Tsukagoshi N., Uda S.;  
 RT "Complete nucleotide sequence of a gene coding for heat- and  
 RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the  
 RT amino acid sequences of three bacterial liquefying alpha-amylases  
 RT deduced from the DNA sequences.";  
 RL J. Biochem. 98:1147-1156(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86195857; PubMed=3009417;  
 RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,  
 RA Carmona C., Requaft C.;  
 RT "Structural genes encoding the thermophilic alpha-amylases of  
 RT Bacillus stearothermophilus and Bacillus licheniformis.";  
 RL J. Bacteriol. 166:635-643(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Shahhoseini M., Ziaei A.A., Ghaemi N., Pourbabaee A.A.;  
 RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-104 FROM N.A.  
 RX MEDLINE=84185455; PubMed=6609154;  
 RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;  
 RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis  
 RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";  
 RL J. Bacteriol. 158:369-372(1984).  
 RN [5]  
 RP SEQUENCE OF 1-29 FROM N.A.  
 RX MEDLINE=89213924; PubMed=2540150;  
 RA Lacide B.M., Chambliss G.H., McConnell D.J.;  
 RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to  
 RT promoter-independent catabolite repression in Bacillus subtilis.";  
 RL J. Bacteriol. 171:2435-2442(1989).  
 RN [6]  
 RP SEQUENCE OF 30-47.  
 RX MEDLINE=82098050; PubMed=6172418;  
 RA Kunz H., Fietzek P.F., Lampen J.O.;  
 RT "N-terminal amino acid sequence of Bacillus licheniformis  
 RT alpha-amylase: comparison with Bacillus amyloliquefaciens and  
 RT Bacillus subtilis enzymes.";  
 RL J. Bacteriol. 149:372-373(1982).  
 RN [7]  
 RP MAPPING OF SUBSTRATE-BINDING SITE.  
 RX MEDLINE=21992788; PubMed=11997021;  
 RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;  
 RT "Action pattern and substrate mapping of Bacillus licheniformis  
 RT alpha-amylase (BLA) with modified maltotriosecarbohydrate substrates.";  
 RL FEBS Lett. 518:79-82(2002).  
 RN [8]  
 RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.  
 RC STRAIN=ATCC 6598;  
 RX MEDLINE=90368748; PubMed=2394736;  
 RA Declerck N., Joyet P., Gaillardin C., Masson J.M.;  
 RT "Use of amber suppressors to investigate the thermostability of  
 RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6  
 RT histidine residues reveal a critical position at His-133.";

RL J. Biol. Chem. 265:15481-15488 (1990).

RP [9] MUTAGENESIS OF ALA-238.

RC STRAIN=ATCC 6598;

RX MEDLINE=96367070; PubMed=8771184;

RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;

RT "Hyperthermostable mutants of *Bacillus licheniformis* alpha-amylase:

RL multiple amino acid replacements and molecular modelling.";

RN Protein Eng. 8:1029-1037 (1995).

[10]

RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;

RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359

RP AND GLU-365.

RC STRAIN=ATCC 6598;

RX MEDLINE=20425100; PubMed=10966804;

RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;

RT "Probing structural determinants specifying high thermostability in

RT *Bacillus licheniformis* alpha-amylase.";

RL J. Mol. Biol. 301:1041-1057 (2000).

[11]

RP MUTAGENESIS OF GLN-293 AND ASN-294.

RC STRAIN=ATCC 6598;

RX MEDLINE=22622182; PubMed=12736372;

RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,

RA Gaillardin C.;

RT "Hyperthermostabilization of *Bacillus licheniformis* alpha-amylase and

RT modulation of its stability over a 50 degrees C temperature range.";

RL Protein Eng. 16:287-293 (2003).

[12]

RP MUTAGENESIS OF TRP-292 AND VAL-315.

RC STRAIN=ATCC 27811;

RX MEDLINE=22797417; PubMed=12915728;

RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;

RT "Alpha-amylase from *Bacillus licheniformis* mutants near to the

RT catalytic site: effects on hydrolytic and transglycosylation

RT activity";

RL Protein Eng. 16:505-514 (2003).

[13]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

RC STRAIN=ATCC 27811;

RX MEDLINE=95182462; PubMed=7877175;

RA Machius M., Wiegand G., Huber R.;

RT "Crystal structure of calcium-depleted *Bacillus licheniformis* alpha-

RT amylase at 2.2-A resolution.";

RL J. Mol. Biol. 246:545-559 (1995).

[14]

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RC MEDLINE=98212915; PubMed=9551551;

RA Machius M., Declerck N., Huber R., Wiegand G.;

RT "Activation of *Bacillus licheniformis* alpha-amylase through a

RT disorder-->order transition of the substrate-binding site mediated

RT by a calcium-sodium-calcium metal triad.";

RL Structure 6:281-292 (1998).

[15]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 330-512.

RC MEDLINE=20384196; PubMed=10924103;

RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,

RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;

RT "Structural analysis of a chimeric bacterial alpha-amylase.

RT High-resolution analysis of native and ligand complexes.";

RL Biochemistry 39:9099-9107 (2000).

[16]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT

RC STRAIN=ATCC 6598;

RX MEDLINE=22538505; PubMed=12540849;

RA Machius M., Declerck N., Huber R., Wiegand G.;

RT "Kinetic stabilization of *Bacillus licheniformis* alpha-amylase through

RT introduction of hydrophobic residues at the surface.";

RL J. Biol. Chem. 278:11546-11553 (2003).

CC -/- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

CC linkages in oligosaccharides and polysaccharides.

CC -/- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

CC

CC -/- SUBUNIT: Monomer.

CC -/- BIOTECHNOLOGY: Used in the food industry for high temperature

CC liquefaction of starch-containing mashes and in the detergent

CC industry to remove starch. Sold under the name Termamyl by

CC Novozymes.

CC -/- MISCELLANEOUS: Able to work at relatively high (alkaline) pH

CC values (up to pH 11) and at high temperatures (up to 100 degrees

CC Celsius).

CC -/- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

CC

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CC EMBL; X03236; CAA36981.1; -

DR EMBL; M38570; AAA22226.1; -

DR EMBL; M13256; AAA22240.1; -

DR EMBL; K01984; AAA22193.1; -

DR EMBL; A9438149; AAO26743.1; -

DR EMBL; M26412; AAA22237.1; -

DR EMBL; A17930; CAA01355.1; -

DR PIR; A91997; ALBSL.

DR PDB; 1BLI; 23-MAR-99.

DR PDB; 1BPL; 17-AUG-96.

DR PDB; 1E3X; 21-JUN-01.

DR PDB; 1E3Z; 24-JUN-03.

DR PDB; 1E40; 24-JUN-03.

DR PDB; 1E43; 21-JUN-01.

DR PDB; 1O80; 03-APR-03.

DR PDB; 1VJS; 12-MAR-97.

DR InterPro; IPR006589; Alp.amyl\_cat\_sub.

DR InterPro; IPR006047; Alpha.amyl\_cat.

DR InterPro; IPR006046; Glyco\_hydro\_13.

DR Pfam; PF00128; alpha-amylase; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

DR SMART; SM00642; Amy; 1.

DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;

KW Signal; 3D-structure.

FT SIGNAL 1 29

FT CHAIN 30 512

FT ACT\_SITE 260 260

FT ACT\_SITE 264 264

FT ACT\_SITE 357 357

FT METAL 133 133

FT METAL 190 190

FT METAL 210 210

FT METAL 212 212

FT METAL 223 223

FT METAL 229 229

FT METAL 231 231

FT METAL 233 233

Query Match 63.0%; Score 1797.5; DB 1; Length 512;

Best Local Similarity 65.0%; Pred. No. 2e-120;

Matches 316; Conservative 69; Mismatches 96; Indels 5; Gaps 2;

QY 1 AAPFNGTWQYFEWYLPDDGTLTKVANEANNSLGTALWLPAYKGTGRSDYGYGY 60

DB 29 AANLNGTLNQYFEWYMPNDGQHWKRLQND SAYLAHSGITAVWIPPAYKGTQADYGYGAY 88

QY 61 DLYDLGEFNQKGTVRTKGTQYQVLOAQAOAHAGMQYADVVDHKGAGTEWDAVE 120

DB 89 DLYDLGEFHQGTVRTKGTGKELQSAIKSLHSRDINVGVDWVNHKGGADATEDVTAVE 148

QY 121 VNPSDRNCEISGTQIOAWTKFDPFGRTGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180

DB 149 VDPADNRNVIAGEHRIKAWTHFHPGRGSTYSDFKWHWHYFDGTDWDSRKLRIYKQ- 207

QY 181 IGKAWDEVDTENGNYDYLMYADLMDHDFEVVTELKNWKWYVNTNTDGFRLDAVKHIK 240

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Db 208 -GRAWDVENSNGNDYLDYADIDYDHPVAAEIKRWGTWYANELQDGRFLDVAKHK 266
Qy 241 FSFPDMLSVRSOTGKPLFTVGEYMSYDINKLHNYITKTGDTMSLFDAPLHKNFYTASK 300
Db 267 FSLRDWNVHREKTKGEMTVAEYQNDLGALENLYNKTNFHSVDFVPLHVFQFHAAS 326
Qy 301 SGGAFTMTLNTLTKMDQPTLAVTFVDNHDTPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 327 QGGGDMRKLNTSVSKPLKAVTFVDNHDTPGQSLSTVOTWFKPLAYAFILTRQEG 386
Qy 361 YPCVFYGDYGI---POYNIPSLKSKTDPLLIARDYVAGTQHDYLDHSDIIGWTRGGT 417
Db 387 YPQVFYGDYGTGDSQREIPALKHKIEPIKARKQYAGQHDYDFPHDILVGTREGDS 446
Qy 418 EKPGSGLAALITDGPCKGKMYGKQHAGKVFYDLTGNRSPTVTINSKGWGEFKVNGGVS 477
Db 447 SVANSGLAALITDGPCKAKMYGVRQNAGETWHDITGNRSEPVVINSEGEFHVNGSV 506
Qy 478 SVMVPR 483
Db 507 SITVQR 512

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## RESULT 4

```

ID AMY_BACAM
AC P00692; STANDARD; PRT; 514 AA.
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
OS glucanohydrolase).
DE Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=IH;
RX MEDLINE=83108808; PubMed=6185474;
RA Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
RA Kaeerlaeinen L.;
RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
RT deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013(1983).
RN [2]
RN SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg F.;
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
RT amylase.";
RL Biochem. J. 185:387-395(1980).
RN [3]
RN SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;
RA Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
RA Soederlund H., Takkinen K., Kaeerlaeinen L.;
RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
RT region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
RL Gene 15:43-51(1981).
RN [4]
RN SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
RT its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170(1987).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkenturg J.P., Bisgaard-Prantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.

```

```

RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC

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EMBL; J01542; AAA22191.1; -
EMBL; V00092; CAA23430.1; -
EMBL; A20154; CAA01489.1; -
EMBL; M18424; AAA22192.1; -
PIR; A92389; ALBSN.
PDB; 1E3X; 21-JUN-01.
PDB; 1E3Z; 24-JUN-03.
PDB; 1E40; 24-JUN-03.
PDB; 1E43; 21-JUN-01.
InterPro; IPR006589; Alp_amy1_cat_sub.
InterPro; IPR006047; Alpha_amy1_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; P00110; ALPHAAMYLASE.
SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 514
FT ACT_SITE 262 262
FT ACT_SITE 292 292
FT ACT_SITE 359 359
FT METAL 133 133
FT METAL 190 190
FT METAL 212 212
FT METAL 225 225
FT METAL 231 231
FT METAL 233 233
FT METAL 235 235
FT METAL 266 266
FT METAL 331 331
FT METAL 438 438
FT METAL 461 461
FT CONFLICT 54 54
FT CONFLICT 64 64
FT CONFLICT 79 79
FT CONFLICT 84 84
SQ SEQUENCE 514 AA; 58403 MW; 3DE66B3FB5CCDE7E CRC64;

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Query Match 62.1%; Score 1773.5; DB 1; Length 514;  
 Best Local Similarity 65.4%; Pred. No. 1e-118;  
 Matches 316; Conservative 57; Mismatches 105; Indels 5; Gaps 2;

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Qy 5 NGTMMQYFEWYLPDDGTLTKVANEANNLSGLITLWLPAYKGTSRSDVGYGVYDLYD 64
Db 33 NGTLQMIFEWYTPNDGQHKRLQNDAEHLSDIGITAVWIPAYKGLSQSDNGYGYDLYD 92
Qy 65 LGFEFNQKGTVRTKYGTAKYQLQAIQAHAAGMAYVADVFDHKGAGDGTWDAVENPS 124
Db 93 LGFEFQKGTVRTKYGTAKYQLQAIQAHAAGMAYVADVFDHKGAGDGTWDAVENPS 152
Qy 125 DRNOEISGTQIQAWTKFDPFGRTGNTSSFKRWYHFDGVDWDSRKLRIYKRGIGKA 184
Db 153 NRNOETSEYQIKAWTDFRFPGRGNTSDFKWHYHFDGADWDSRKLRIYKRGIGKA 212

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QY 185 WDNEVDTEGNYDYLMYADLMDHPEVVTTELKNGKGYVNTTNDGRLDVAHKHKSFF 244
Db 213 WDWVSSGNGYDYLMYADLMDHPEVVTTELKNGKGYVNTTNDGRLDVAHKHKSFF 272
QY 245 PDWLSYVRSOTGKPLFTVGEYWSVDINKLHNYLTKDTGWSLDPALPHNKFYTASKSGGA 304
Db 273 RDWQAVRQATGKEMFTVAETWQNNAGKLENLTKTSFNSQSVFDPVPHFNQAASSGGG 332
QY 305 FDMRTLMTLMDKQDPTLAVTFVDNHDTEPQALQSWVDWPFKPLAYAFILTRQEGYPCV 364
Db 333 YDMERLLDGTWVSRHPEKAVTFVENHDTQPGSLESTVQWFKPLAYAFILTRQEGYPCV 392
QY 365 FYGDIYGI-----PQYNPSLKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 393 FYGDMYTKGTSPK-EIPSLKDNIEPILKARKEYAYGPHDYIDHPDVIWGTREGDSAA 451
QY 421 GSGLAALITDPPGSGKMYVKGOKHAGKVFYDLTGNSRDTVTINSDGWGEFKVNGSVSW 480
Db 452 KSGLAALITDPPGSGKMYAGLKNAGETWYDITGNRSDDTVKIGSDGHWGEFHVNDGVSIIY 511
QY 481 VPR 483
Db 512 VQK 514

RESULT 5
AMY2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase).
GN AMYA OR STM1963.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JW1103;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Lr2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT Lr2.";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=JW1103;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [4]
RP SEQUENCE OF 476-494 FROM N.A.
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIIb, including a

```

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RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
CC EMBL; L01643; AAA27110.1; -.
CC EMBL; AB008787; AAL20875.1; -.
CC EMBL; M85241; AAA27079.1; -.
CC EMBL; L13280; AAA71970.1; -.
CC PIR; B45738; B45738.
CC HSSP; P06278; IVJS.
CC StyGene; SGI0011; amyA.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 462 L -> S (IN REF. 1).
FT SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5E47C CRC64;
Query Match 38.9%; Score 1110.5; DB 1; Length 494;
Best Local Similarity 44.0%; Pred. No. 1.2e-71; Mismatches 176; Indels 17; Gaps 5;
Matches 216; Conservative 82;
QY 5 NGTMQYFEWYLPDDGTLTKVANEANNLSLIGITALLMPPAYKGTSSRS-DVGYGYDYLY 63
Db 3 NPTLLQYFHWYYPDGGKLSWSELAERADGLDGINWMLPPACKGASGGYSGYDYDLY 62
QY 64 DLGEFNQKGTVTYKGTAKYLOAQIAHAAGQVYADVFDHKGADTEWDAVEVNP 123
Db 63 DLGEFDQKGTIATKYGDKRQLLTALDALKNNIAVLDDVVVNHKMGADKERRIVQVNO 122
QY 124 SRNQEISGTYOIOAWTKPFPGRGNTYSSFKRWYHFDGVDWDESRKLSRYKPRG--I 181
Db 123 DRTQIDDDNIICEGWTRITFFPARAGQYNSFNFDVHCFSGIDHIEPNDEGDFKIVNDYT 182
QY 182 GKAWDEVDTEGNYDYLMYADLMDHPEVVTTELKNGKGYVNTTNDGRLDVAHKHIF 241
Db 183 GDGNDQVDDENGNFDYLMGENIDFRNHAVTEIKYWARVWMEQTHCDGRLDVAHKHIA 242
QY 242 SFFPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYLTKDTGWSLDPALPHNKFYTASKS 301
Db 243 WFKYKIEWHVQAVAPKPLFIVAIEYWSHVEDLQTVTDQVDGKTMFLDPAQMKFHEASRQ 302
QY 302 CGAFDMRTLMTLMDKQDPTLAVTFVDNHDTEPQALQSWVDWPFKPLAYAFILTRQEGY 361
Db 303 GAEYDMRHIPTGLTLEADPFHATVILVANHDTPQLQALEAPVFPWFKPLAYAILLRENGV 362
QY 362 PCVFYGDYGYGIP-----QYNIPSLKSIDPLLIARRDYAYGTQHDYLDHSDIIG 410
Db 363 PSVFYPDLYGASVYEDSGENGETCRDMPVI-NQLDRLLILARQRFAGHIGITLFDHPNCA 421
QY 411 WTREGGTEKPGSGLAALITDPPGSGKMYVKGOKHAGKVFYDLTGNSRDTVTINSDGWGEF 470

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Db 422 FSRSGTEENP--GCVVVLSNGDGEKTLILLGDNVANKYTRDFLGNRDEYVVTNDQGEATP 479

Qy 471 KVRGGSVSVWV 481

Db 480 FCNAGSVSVWV 490

# RESULT 6

AMV2 ECOLI  
ID AMV2 ECOLI STANDARD; PRT; 495 AA.  
AC P26612; P78072;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan  
DE glucanohydrolase).  
GN AMYA OR B1927.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JAL1.  
RX MEDLINE=93015717; PubMed=1400215;  
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;  
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";  
RL J. Bacteriol. 174:6644-6652(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Aiba H., Baba T., Fujita K., Hayaashi K., Inada T.,  
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,  
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,  
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
RN [4]  
RP SEQUENCE OF 1-5 FROM N.A.  
RC STRAIN=JAL1;  
RX MEDLINE=92407478; PubMed=1527488;  
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;  
RT "Subdivision of flagellar region III of the Escherichia coli and  
RT Salmonella typhimurium chromosomes and identification of two  
RT additional flagellar genes.";  
RL J. Gen. Microbiol. 138:1051-1065(1992).  
RN [5]  
RP SEQUENCE OF 475-495 FROM N.A.  
RC STRAIN=JAL1;  
RX MEDLINE=93381452; PubMed=8371104;  
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;  
RT "Organization of the Escherichia coli and Salmonella typhimurium  
RT chromosomes between flagellar regions IIIa and IIb, including a  
RT large non-coding region.";  
RL J. Gen. Microbiol. 139:1401-1407(1993).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
CC linkages in oligosaccharides and polysaccharides.  
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
CC -1- SUBUNIT: Monomer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; L01642; AAA23810.1; --  
CC EMBL; AE000285; AAC74994.1; --  
CC EMBL; D90833; BAA15755.1; --  
CC EMBL; M85240; -- NOT ANNOTATED\_CDS.  
CC EMBL; L13279; AAA82575.1; --  
CC PIR; D64956; A45738.  
CC HSP; P06278; IVJ5.  
CC EcoGene; EG11387; amyA.  
CC InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
CC InterPro; IPR006047; Alpha\_amy1\_cat.  
CC Pfam; PF00128; alpha-amylase; 1.  
CC SMART; SM00642; Amy; 1.  
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
KW Complete proteome.  
FT ACT\_SITE 235 235 BY SIMILARITY.  
FT ACT\_SITE 265 265 BY SIMILARITY.  
FT ACT\_SITE 332 332 BY SIMILARITY.  
FT METAL 104 104 CALCIUM (BY SIMILARITY).  
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY  
FT SIMILARITY).  
FT CONFLICT 19 20 KL -> SS (IN REF. 1).  
FT CONFLICT 109 109 A -> V (IN REF. 1).  
FT CONFLICT 149 149 Q -> E (IN REF. 1).  
FT CONFLICT 234 234 L -> I (IN REF. 1).  
SQ SEQUENCE 495 AA; 56639 MW; 26AFP6797DDA54D6 CRC64;  
  
Query Match 37.6%; Score 1074.5; DB 1; Length 495;  
Best Local Similarity 42.9%; Pred. No. 4.4e-69;  
Matches 210; Conservative 83; Mismatches 182; Indels 15; Gaps 4;  
  
Qy 5 NGTMMQYFEWYLPDDGTLTKVANEANLSSGLTALWLPAYKGTSSR-DVGVGVVDLY 63  
Db 3 NPTLLQCFHWYYPGGKLPALRADGDFNDIGINWMLPYPAYKASGGYSGVSYDLF 62  
Qy 64 DLGEFNGKGVTRKYGTQAOYLQIAHAAGQVADVVDVHKGGADGTETWDAVWNP 123  
Db 63 DLGEFDKGSIPYKYGKQAQLLAIDAKNDIAVLDDVVNHWGADEKAEIRVQVNA 122  
Qy 124 SDRNQETSGTYQIAWTKFPDPCRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG--I 181  
Db 123 DDRQTQIDEEIIECEGWTRYTFPARAGYSQFIWDFKCFSGIDHNPEDGIFKIVNDYT 182  
Qy 182 GKAWDEVDTENGNYDLYADLMDHPFVTELKWKGVVNTTNDGRLDAVKHKP 241  
Db 183 GEGNDQVDDDELGNFDYLMGENIDFRNHAFTVEIKYWARWMEQTQCDGFLDAVKHPA 242  
Qy 242 SFPDMLSYVRSQTGKPLFTVGEVSYDINKLHNYITKDTWSLFDAPLHNKFTASKS 301  
Db 243 WFKWEIHEVQEVAPKPLFVAEYWSHEVDKLTQYIDQVEGKTMFLDAPLQMKHEASRM 302  
Qy 302 GGAFDMRTLMTNTLMKDDQPTLAVTFVDNHDTEFGAQLQSWDVPWFKPLAYAFILTRQEGY 361  
Db 303 GRDYDMTQIFTGTLVEADPFHVLTVANHDTPQLQALEAPEVPWFKPLAYALLRENGV 362  
Qy 362 PCVPFYGYGYPQVNIIPS-----LASKKDPLLIARDVAYGTQHDYLDHSDLIIGW 411  
Db 363 PSVFYPLDYGHAHYEDVGGGQGTYPIDMPIIEQLDELILARQFAHGQYTLFFDHPNCIAF 422  
Qy 412 TREGTEKPGSGLAALITDGGGSKWYVKGQHAGKVFYDLTGNRSSTVATINSQWGEFK 471  
Db 423 SRSGTDEFP--GCVVVMSNGDDGKEKTHLGENYGNKTRDFLGNRQERVVDENGEATFF 480

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QY 472 VNGGSVSVWV 481
Db 481 CNGGSVSVWV 490

RESULT 7
CDGT_BACSP
ID CDGT_BACSP STANDARD; PRT; 713 AA.
AC P30921;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGT.
OS Bacillus sp. (strain 17-1).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
RX MEDLINE=90257592; PubMed=2534600;
RA Kaneko T., Song K.B., Hamamoto T., Kudo T., Horikoshi K.;
RT "Construction of a chimeric series of Bacillus cyclomaltodextrin
RT glucanotransferases and analysis of the thermal stabilities and pH
RT optima of the enzymes.";
RL J. Gen. Microbiol. 135:3447-3457(1989).
CC -! CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -! COFACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -! SUBUNIT: Monomer.
CC -! MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -! SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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EMBL; M28053; AAA22310.1; -.
HSPSP; P43379; 1CDG.
InterPro; IPR006589; Alp_amy1_cat_sub.
InterPro; IPR006048; Alpha_amy1_C.
InterPro; IPR006047; Alpha_amy1_cat.
InterPro; IPR002044; CBD_4.
InterPro; IPR006046; Glyco_hydro_13.
InterPro; IPR007110; Ig-like.
InterPro; IPR002909; IPT_TIG.
Pfam; PF00129; alpha-amy1ase_1.
Pfam; PF02806; alpha-amy1ase_C; 1.
Pfam; PF00686; CBM_20; 1.
Pfam; PF01833; TIG; 1.
PRINTS; PR00110; ALPHAAMYLASE.
ProDom; PD001568; CBD_4; 1.
SMART; SM00642; Amy_1.
SMART; SM00632; Amy_C; 1.
Transferase; Glycosyltransferase; Calcium-binding; Signal.
FT SIGNAL 1 27
FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 28 165 A1.
FT DOMAIN 166 229 B.
FT DOMAIN 230 433 A2.
FT DOMAIN 234 522 C.
FT DOMAIN 523 609 D.
FT DOMAIN 610 713 E.
FT ACT_SITE 256 256 BY SIMILARITY.

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FT ACT_SITE 284 284 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT METAL 54 54 CALCIUM 2 (BY SIMILARITY).
FT METAL 56 56 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 59 59 CALCIUM 2 (BY SIMILARITY).
FT METAL 60 60 CALCIUM 2 (BY SIMILARITY).
FT METAL 78 78 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 80 80 CALCIUM 2 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 1 (BY SIMILARITY).
FT METAL 217 217 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 226 226 CALCIUM 1 (BY SIMILARITY).
FT METAL 260 260 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT DISULFID 70 77 BY SIMILARITY.
SQ SEQUENCE 713 AA; 77389 MW; D13AEF6C507FF45E CRC64;

Query Match 11.0%; Score 313; DB 1; Length 713;
Best Local Similarity 24.7%; Pred. No. 8.6e-15;
Matches 135; Conservative 82; Mismatches 188; Indels 142; Gaps 29;

QY 19 DGTL-----WTKVANEANN--LSSLGITLWLP--AYKGTSRSDVGYGYDL 62
Db 67 DGTCTNRLRYCGDMQGIINKINDGYLTGCVTAIWISQPVENIYSVINSGVNTAYHG 126
QY 63 YDLGEFENKGTVRTKYTKAQVLAQAAHAGMOYADVDFHKGGA--DGTWWDVAVE 120
Db 127 YWARDPK---TNPAYGTIADFQNLIAAAHAKNKKVIIDFAFNHTSPASLDQPSFAENGK 183
QY 121 VNPDRNOEISGTQIQOAMTKDFPFGNGNTYSFKRWYHFDGVDWDESKLSRYKPRG 180
Db 184 LYNNGRDE---GGY-----TNDTNLF---HHNGGTDFS-----211
QY 181 IKGAMDWEVDTEGNYDYLM-YADLMDHPEVVTLEKNWGWYVNTTIDGFRDLDAVRHI 239
Db 212 -----TTENGIVKKNLYDLADLNHNNTVDTYLDKAIKWLD-LGIDGIRMDAVKGM 261
QY 240 KFSFPDMLSVRSQTGKPLFTVGEYWSVDINKL--HNYITKDTGTMISLFDAPLHNKPYT 297
Db 262 PFGWKQSFPMVNNY--KPVFTFGE-WFLGVNEVSAENHKFANVSGMSLLDPRFAQKVRQ 318
QY 298 ASK--SGGAFFDMRTLMTNTL-----MKDQPTLAVTFVDNHDTE---PGQALQSWVDWPFK 347
Db 319 VFKNDTNMYGLKSMLEGSATDYAQMEDQ---VTFIDHDMERFHNSANRKLQEQ---371
QY 348 PLAYAFILTRQEGYPCVGYDYGYIPOY-----NIPS-----LKSIDPL 387
Db 372 --ALAFITLT-SRGVPAI-----YGTQYMSGNDPDNRARIPSFSTTTTAYQVSKKLAPL 424
QY 388 LIARRDYAGTQHDYLDHSDIIGWTREGGTE-----KPGSLAALITDGPSSKW 437
Db 425 RKSNPALAYGTTQERWINNDVLIYERKFNNAVAVANRNNTSASITGLVTSLPAGS--482
QY 438 MYVGKHAGKVFYDLTGN--RSDTVTINSDGWGE-FKVGGSVSVW-VPRKTTVSTIAR-492
Db 483 -----YTDVLGGLNGNLTVCSSGGSASITFLAAGGTAVWQYTTAVTAPTIGHV 531
QY 493 -PIITRP 498
Db 532 GPMMAKP 538

RESULT 8
AMVB_PAEPO
ID AMVB_PAEPO STANDARD; PRT; 1196 AA.
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amy1ase precursor [includes: Beta-amy1ase (EC 3.2.1.2);
DE Alpha-amy1ase (EC 3.2.1.1)].

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QY 461 TINSOGW-----GEF-----KVGSGSVVW-PRKTTVST 489
DB 1141 VFNNWNSQRTTIGNFDNLNGRLTNQLSNDVSQVINGSIITVLAPKEVKVFT 1195

RESULT 9
AM3A_ORYSA
ID AM3A_ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
CC -!- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
CC -!- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurones cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56336; CAA39776.1; -.
DR PIR; S14958; S14958.
DR HSSP; P04063; IAVA.
DR Gramene; P27932; -.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006047; Alp_amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 440
FT ACT_SITE 207 207 ALPHA-AMYLASE ISOZYME 3A.
FT ACT_SITE 315 315 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT METAL 145 145 CALCIUM 1 (BY SIMILARITY).
FT METAL 155 155 CALCIUM 2 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 3 (BY SIMILARITY).
FT METAL 169 169 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT METAL 170 170 CALCIUM 1 (BY SIMILARITY).
FT METAL 171 171 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).

FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT METAL 176 176 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 10.6%; Score 302.5; DB 1; Length 440;
Best Local Similarity 28.4%; Pred. No. 2.7e-14;
Matches 117; Conservative 47; Mismatches 147; Indels 101; Gaps 21;

QY 8 MMQYFEW-YLPDDGTLWTKVANEANLSSLGITALLMLPAYKGTSTSDVGYVDLYDLG 66
DB 31 LFGFNFNDSWKKQGWYNMLKQDQVGIASAGVTHVWLPPTTH--SVSPQGYMPGRLYDLN 88
QY 67 EFNQKGTVRTKYGTAKYQLQAIQAAHAAQGVVADVVDHKGAGDGTWVDAVEVNPSTR 126
DB 89 -----ASKYGTKAELSLTAAFAKGIKCVADIVNHRCAD----- 125
QY 127 NOISITGYIQAWTKFDFPGRNTYSSFKRWYHFDGVDWDSRKLRIYKFR-GIGKAW 185
DB 126 -KDRGKVYCI-----FKGGGPR-----GCLDWGSPMICCDTQYSDGTGHR- 165
QY 186 DWEVDTEGNYDYLWYADLMDHPEVVTTELKNWGWVNTTNDGERLDAVKHKESFPP 245
DB 166 -----DT---GADFAAAPDIDLNLPLVQRELSDWLRRLRDVGDGWRDLFAKGYSAVA- 217
QY 246 DWLSYVRSQTGKPLFTVGEYW---SYD-----INKLHNYITKTDGTMSLFDAP 290
DB 218 --RTYV--QNAKPSFVVAISWLSYDGGKPAANDGQORQELVNWVWQVGGPATAFDFT 273
QY 291 LHNKFTASKSGGAFDMRTMTNTLMKD-----OPTLAVTFVDNHDTPFQALQSW 341
DB 274 TKGILQSAVQ--GELWFRMD-----KDGKAPGMIGWPEKAVTFVDNHD--GSTQRMW 323
QY 342 VDPWFKP-LAYAFILTRQEGYCVFYGVYGPQYNIPSLKSKIDILLIARR 392
DB 324 PFPDSKVLGYAYILT-HPGVPCIFYDQVF---DMN---LKQEINALAATRK 368

RESULT 10
CDGT_BACS8
ID CDGT_BACS8 STANDARD; PRT; 713 AA.
AC P17692;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltoextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting
DE amylase).
OS Bacillus sp. (strain B1018).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1417;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
RX MEDLINE=90147765; PubMed=1689153;
RA Itokor P., Tsukagoshi N., Udaoka S.;
RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
RT Bacillus sp. B1018 and its strong homology to the cyclodextrin
RT glucanotransferase genes.";
RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
CC -!- FUNCTION: This endo-type adsorbable amylase is capable to
CC digest raw starch.
CC -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -!- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC
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CC EMBL; M33302; AAA22239.1; -.
CC EMBL; D90112; BAA14140.1; -.
DR PIR; S09196; S09196.
DR HSP; P43379; ICDG.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR002909; IFT_TIG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG_1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
DR TRANSFERASE; Glycosyltransferase; Calcium-binding; Signal.
FT SIGNAL 1 27
FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT ACT_SITE 256 256 BY SIMILARITY.
FT ACT_SITE 284 284 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT METAL 54 54 CALCIUM 1 (BY SIMILARITY).
FT METAL 56 56 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 59 59 SIMILARITY).
FT METAL 59 59 CALCIUM 1 (BY SIMILARITY).
FT METAL 60 60 CALCIUM 1 (BY SIMILARITY).
FT METAL 80 80 CALCIUM 1 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 2 (BY SIMILARITY).
FT METAL 217 217 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 226 226 SIMILARITY).
FT METAL 260 260 CALCIUM 2 (BY SIMILARITY).
FT METAL 260 260 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 713 713 AA; 77420 MW; 85F616DA687B888 CRC64;
SQ SEQUENCE 713 AA; 77420 MW; 85F616DA687B888 CRC64;

Query Match 10.6%; Score 302; DB 1; Length 713;
Best Local Similarity 24.7%; Pred. No. 5.2e-14;
Matches 136; Conservative 80; Mismatches 205; Indels 130; Gaps 29;

QY 2 APFNGTWQVFEWYLPDGTGLTKVANEANN--LSSLGITALLWLP--AYKGTSSDV 55
DB 64 AAFDGTCTN-LRLYCGD---WQGIINKINDGYLTGMVTAIWISQPVENIYIISGV 119
QY 56 GYGVYDLYLGEFNQKGTVRTKYTKAQYLQAIQAHAAGQVYADVVDHKGADGTEW 115
DB 120 NNTAYHGYWARDPKK---TPAYGTIADFQNLIAAHAHAKIKVIIDFAPNHTSPASSDQP 176
QY 116 VDAVEVNPDRNQBEISGTQIQIOWTKDFPGRGNWTYSFKRWTHFGDWDSEKLSRI 175
DB 177 SFAENGRLYD-NGTLGGY-----TNDTQNLF-----HHNGGTDPS----- 211
QY 176 YKFRGICKANDWEVDTEGNYDLYLWADLMDHDEEVUTE--LKNWGWYNTNTNIDGRL 233
DB 212 -----TTENGYYKNL-YDLADLNHNNSDVSVDYLDKAIKWLID-LGIDGIRM 255
QY 234 DAVKHIFSPFPDPLSVRSQTKPLFTVGSYWDYNKLN--HNYITKDTGMSLLDAPL 291
DB 256 DAVKHPFGQKSPMAAVNNY--KPVTFGE-WFLGVNEVGPENHKNANESGMSLLDFRP 312
QY 292 HNKFYTA--SKSGAGFDMRTLMNTNL-----MKDQPLAVTFVDNHDTEPQALQSWVDP 344
DB 313 AQKRVQVRFDNTDMNYGLKAMLEGAADYAQVDDQ-----VTFIDNHDWERPHAGNANRRK 368
QY 345 WFKELAVAFILTRREGVPCVGYDYGIPQY-----NTPSLKS-----KI 384
DB 369 LEQALAFTLILAR---VPAI-----YGTGEQYMSGGTDPDNRRIPSPFSTTAYQVQKL 421

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QY 385 DPLLIARDYAYGTQHDYLDHSDIIGWTRGGT-----EKPGSLAALITDPCG 433
DB 422 APLRKNPAIAYGSTOERWINNDVLIYERKFGSNVAVVAVNRNLNAPAS-ISGLVTSLPQ 480
QY 434 GSKWMYVGKQHAGKVFYDLTGN--RSDTVTINDG-WGEFKVNGSVSW-VPRKTTVST 489
DB 481 GS-----YNDVLGGLNGTLVGGGAASFTLAAGGTAVWQYTAATATPT 527
QY 490 IAR--PITTRP 498
DB 528 IGHVGPMMAKP 538

RESULT 11
CDGU_BACCI
ID_CGU_BACCI STANDARD; PRT; 713 AA.
AC P43379;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
OS Bacillus circulans
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 28-37, AND X-RAY CRYSTALLOGRAPHY (2.0
RP ANGSTROMS).
RC STRAIN=251;
RX MEDLINE=94149761; PubMed=8107143;
RA Lawson C.H., van Montfort R., Strokopytov B., Rozeboom H.J.,
RA Kalk K.H., de Vries G.E., Penninga D., Dijkhuizen L., Dijkstra B.W.;
RT "Nucleotide sequence and X-ray structure of cyclodextrin
RT glycosyltransferase from Bacillus circulans strain 251 in a maltose-
RT dependent crystal form."
RL J. Mol. Biol. 236:590-600(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC STRAIN=251;
RX MEDLINE=96094317; PubMed=7493956;
RA Knegtel R.M.A., Strokopytov B., Penninga D., Faber O.G.,
RA Rozeboom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.;
RT "Crystallographic studies of the interaction of cyclodextrin
RT glycosyltransferase from Bacillus circulans strain 251 with natural
RT substrates and products."
RL J. Biol. Chem. 270:29256-29264(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=97115811; PubMed=8955113;
RA Penninga D., van der Veen B.A., Knegtel R.M.A., van Hijum S.A.F.T.,
RA Rozeboom H.J., Kalk K.H., Dijkstra B.W., Dijkhuizen L.;
RT "The raw starch binding domain of cyclodextrin glycosyltransferase
RT from Bacillus circulans strain 251."
RL J. Biol. Chem. 271:32777-32784(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR.
RC STRAIN=251;
RX MEDLINE=96264806; PubMed=8672460;
RA Strokopytov B., Knegtel R.M.A., Penninga D., Rozeboom H.J., Kalk K.H.,
RA Dijkhuizen L., Dijkstra B.W.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a
RT maltotriose inhibitor at 2.6-A resolution. Implications for product
RT specificity."
RL Biochemistry 35:4241-4249(1996).
CC -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -!- COFACTOR: Binds 2 calcium ions per subunit.
CC -!- SUBUNIT: Monomer.
CC -!- DOMAIN: May consist of two protein domains: the one in the amino-
CC terminal side cleaves the alpha-1,4-glucosidic bond in starch, and
CC the other in the C-terminal side catalyzes other activities,
CC including the reconstitution of an alpha-1,4-glucosidic linkage
CC for cyclizing the maltooligosaccharide produced.

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Db 138 AYGTWQDFKNIIDTAHAKNIKIIVDFAPNHTSPASSDDPSFAENGRLYD-NGNLLGGY-- 194
Qy 137 QAWTKFDPGRGNTVSSSKFWYHFDGVDWDESRKLSRIYKFRIGKAWDEWDTENGNY 196
Db 195 -----TNDTONLF-----HYGGTDFS-----TIENGII 218
Qy 197 DYLW-YADLMDHPVTELVKNGWKYVNTTNDIGFRLDAVKHKFSFPDPWLSYVSQT 255
Db 219 KNLVDLADLNHNSSVDVYLKDAIKWLD-LGVGIRVDAVKHMPFGWQKSPMSTINNY- 276
Qy 256 GKPLFTVGEYSYDINKL-----HNYITKDTGMSLFDAPLNKPYTA--SKSGAFDMRT 309
Db 277 -KPVNFGE-WFLGVNEISPEYHOFANESG--MSLLDFPAQKARQVFRDNTDNYGLKA 332
Qy 310 LMTWT-----LMKQDPTLAVTVFNHDETPCQALQSWDPWFKPLAVAFILTRQEGYPCV 364
Db 333 MLEGEVDYAQVNDQ-----VTFIDHMERHFTSNG--DRKLEQALAFILT-SRGVPAI 385
Qy 365 FYGDIYGIPOY-----NIPSLKS-----KIDPLLIARRDYAYGTQHDYLD 404
Db 386 ----YIGSEQYMGNDPDRARIPSPSTTTTAYQVIQKLAFLRKSNPALAYGSTQERWI 441
Qy 405 HSDLIIGTREGGT-----EKPGSLAALITDGPQSGKMYGVKQHAGKVFVDLT 453
Db 442 NNDVILVERKGNVAVVAINRNMNTPAS-ITGLVTSLPQGS-----YNDVL 487
Qy 454 GN--RSDVTINSDG-WGEFKVNGSVSMVPRKTTVST 489
Db 488 GGILNGNTLVGAGGAASNTFLAPGCTAVW--QYTTDAT 524

RESULT 13
CDGT_BACLI
ID _CDGT_BACLI STANDARD; PRT; 718 AA.
AC P14014,
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltodextrin glucanotransferase precursor (BC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGTA
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=90174931; PubMed=2137908;
RA Hill D.E., Aldape R., Rozzell J.D.;
RT "Nucleotide sequence of a cyclodextrin glucosyltransferase gene,
RL cgtA, from Bacillus licheniformis.";
CC Nucleic Acids Res. 18:199-199(1990).
CC -I- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -I- COPACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -I- SUBUNIT: Monomer.
CC -I- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; X15752; CAA33763.1; --
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DR PIR; S15920; ALBSMX.
DR HSPP; P30920; 1CGT.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD 4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBM 20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD 4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy; C; 1.
DR Transferase; Glycosyltransferase; Calcium-binding; Signal.
KW TRANSFERASE; BY SIMILARITY.
FT SIGNAL 1 34
FT CHAIN 35 718
FT DOMAIN 35 172
FT DOMAIN 173 236
FT DOMAIN 237 440
FT DOMAIN 441 528
FT DOMAIN 529 614
FT DOMAIN 615 718
FT ACT_SITE 258 258
FT ACT_SITE 291 291
FT ACT_SITE 362 362
FT METAL 61 61
FT METAL 63 63
FT METAL 66 66
FT METAL 67 67
FT METAL 85 85
FT METAL 87 87
FT METAL 173 173
FT METAL 224 224
FT METAL 233 233
FT METAL 267 267
FT DISULFID 77 84
FT SEQUENCE 718 AA; 78002 MW; B3CDE14A81D5DC4E CRC64;

Query Match 10.0%; Score 286; DB 1; Length 718;
Best Local Similarity 23.1%; Pred. No. 7,2e-13;
Matches 138; Conservative 78; Mismatches 196; Indels 186; Gaps 30;

Qy 2 APFNGTMMQYFEWYLPDDGTTLWTKVANEANN--LSSLGITALLWLPAA-----YKG- 49
Db 71 AAFDGTCSN-LKLYCGGD---WQGLVKNKINDYFSDLGVTALWISQPVENIPATINYSGV 126
Qy 50 TSSRSDVGYGVVDLYDLGEBFNQKGTVRTKGYKAQYLOIAHAAAGMOVYADVDFHRGG 109
Db 127 TNTAYHGYWARDFKKINPY-----FGTWTDQNLVTTAAHAKGIKIIDFAPNHTSP 177
Qy 110 ADGTWDAVEVNPDSRNRQEIISGTYQIQAWTKFDPGRGNTYSSFKWRYHFDGVDWDES 169
Db 178 AMETDTSFAENGKLYDNGNLVGG-----YTNDTNGY-----FHNGGSDFS-- 218
Qy 170 RKLRIYKFRGIGKAWDEWDTENGNYDYLW-YADLMDHPVTELVKNGWKYVNTTNI 228
Db 219 -----TLENGIYKNLVDLADLNHNSTIDTYFKDAIKLWLD-MGV 257
Qy 229 DGFRLDAVKHKFSFPDPWLSYVSQTKPLFTVGEYSYDINKLHNYITKDTGT----- 283
Db 258 DGIIRDVAVKHMPFGWQKWNMSIVAH--KPVTFGEWF-----LGSAAADPNDTDFANE 309
Qy 284 --MSL-----FDAPLNKPYTASKSGAFDMRTLMTNTL-----MKDQPTLAVTVFNHDE 332
Db 310 SGMSLLDPRFNSAVRNRDNTSNWYALD--SMLTAAADYNQVNDQ-----VTFIDNHDM 363
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RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;  
 RL "Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";  
 CC Catalytic Activity: Endohydrolysis of 1,4-alpha-glucosidic  
 CC linkages in oligosaccharides and polysaccharides.  
 CC -I- COFACTOR: Binds 3 calcium ions per subunit (By similarity).  
 CC -I- SUBUNIT: Monomer (By similarity).  
 CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
 CC  
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 CC  
 DR EMBL; X53049; CAA37217.1; -;  
 DR EMBL; X73301; CAA51734.1; -;  
 DR PIR; S10514; S10514.  
 DR HSP; P04063; LAVA.  
 DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
 DR InterPro; IPR006047; Alpha\_amy1\_cat.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR SMART; SM00642; Amy; 1.  
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;  
 KW Signal.  
 FT SIGNAL. 1 23 PROBABLE.  
 FT CHAIN 24 421 ALPHA-AMYLASE.  
 FT ACT SITE 201 201 BY SIMILARITY.  
 FT ACT SITE 309 309 BY SIMILARITY.  
 FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).  
 FT METAL 130 130 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).  
 FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).  
 FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).  
 FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY  
 FT METAL SIMILARITY).  
 FT METAL 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).  
 SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;  
 Query Match 9.9%; Score 283; DB 1; Length 421;  
 Best Local Similarity 26.3%; Pred. No. 6.1e-13;  
 Matches 103; Conservative 48; Mismatches 142; Indels 98; Gaps 17;  
 QY 8 MNOYFEWLPDDGTLWTKVANEANNLSLGLTALWLPAYKTSRSDVGVGYDYLIGE 67  
 DB 26 LFGQFNWESSKGGWYNSLKNIPDLNAGITHVWLP--PSQSVSEGLPGRLYDLD- 82  
 QY 68 FNQKGTVRTYKTYQAOIAQAAHAGMOVYADVDFDHKGG--ADGTWVDAVEVNPDS 125  
 DB 83 -----ASKVGSKNELSLIAAFHEKGIKCLADIVINHRTAERKDGRIYCIIEGGTPD 135  
 QY 126 RNOEISCTYQIQAWTKFDFPGRGNTYSSFKRWYTHFDGVWDSEKLSRIYKFRGIGKAW 185  
 DB 136 SRQDWGSPFCRDDTAYS-DGTGNDS-----GEGY 165  
 QY 186 DWEVDTENGYDLYMADLMDH--PEVVTLEKNWKKWYNTNIDGPRLDVAKHKFSF 243  
 DB 166 D-----AAPDIDLHPQVQRELSMMNLKTEIGFDGWRDFVK-----GY 206  
 QY 244 FPQWLSYVRSGTKPLFTVGEYW---SY-----DINK--LHNYITKDTGMSLFD 288  
 DB 207 APS-ISKIYNEQTKPDAVEGKWDISYQDGCKPNYNQDSHRGALVNWVSAGGAIATFD 265  
 QY 289 -----APLHNKFTASKSGGAFDMRTLMNTLMKDKQPTLATVFDVNNHDTPEGQALQS 340  
 DB 266 FTTKGILQAQVQGLWRLIDPNG-----KPPGMIGVKPENAVTFIDNHD--GSTQRL 316

Qy 341 WVDPMFKPL-AYAFILTRQSGYPCVCFYGDY 370  
 Db 317 WPFPSDKVMQGYAYILT-HPGTSPSIFYDHFF 346  
 Search completed: October 7, 2004, 00:13:20  
 Job time : 11.0324 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 49.3774 Seconds  
(without alignments)  
3290.816 Million cell updates/sec

Title: US-09-925-576C-6  
Perfect score: 2854  
Sequence: 1 AAPFNGTMQYFEWYLPDDG.....TRPWTGEFVWTEPRILVAMP 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL\_25.\*
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phage.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_virus.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_unclassified.\*
  - 15: sp\_rvirus.\*
  - 16: sp\_bacteriap.\*
  - 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2840	99.5	549	2	Q31193
2	2818	98.7	549	2	Q9KW16
3	2658	93.1	521	2	P71034
4	2404	84.2	613	2	Q59222
5	1910.5	66.9	516	2	Q82839
6	1841.5	64.5	533	2	Q8A054
7	1837.5	64.4	519	2	Q8RQ78
8	1829.5	64.1	513	16	Q81AS4
9	1827.5	64.0	513	16	Q81XJ4
10	1700	59.6	507	16	Q87HG6
11	1618	56.7	501	2	Q93148
12	1345.5	47.1	492	16	Q8YU21
13	1322.5	46.3	481	16	Q89YF1
14	1315	46.1	484	16	Q97Q49
15	1311	45.9	484	16	Q8DFC8
16	1296	45.4	488	16	Q8E0M2

17	1295	45.4	488	16	Q8E696	Q8E696 streptococc
18	1278.5	44.8	493	2	Q03657	Q03657 bacillus c1
19	1268	44.4	486	16	Q8DT08	Q8DT08 streptococc
20	1260	44.1	484	2	O50583	O50583 streptococc
21	1244	43.6	485	2	O53786	O53786 streptococc
22	1237	43.3	486	2	O68875	O68875 streptococc
23	1229	43.1	491	16	Q9CG59	Q9CG59 lactococcu
24	1101.5	38.6	494	16	Q8Z5S5	Q8Z5S5 salmonella
25	1078.5	37.8	506	16	Q8U916	Q8U916 agrobacteri
26	1077.5	37.8	495	16	Q8FGL8	Q8FGL8 escherichia
27	1074.5	37.6	495	16	Q8XBB6	Q8XBB6 escherichia
28	1066.5	37.4	495	16	Q7UAB0	Q7UAB0 shigella fl
29	1064.5	37.3	495	16	Q83R40	Q83R40 shigella fl
30	967	33.9	529	3	Q877B1	Q877B1 aspergillus
31	486	17.0	461	1	Q8NKR5	Q8NKR5 thermococcu
32	483.5	16.9	461	1	Q8NKR4	Q8NKR4 thermococcu
33	482	16.9	469	1	O50200	O50200 thermococcu
34	481	16.9	461	1	O33476	O33476 pyrococcus
35	475	16.6	460	1	O08452	O08452 pyrococcus
36	475	16.6	473	17	Q8U319	Q8U319 pyrococcus
37	474	16.6	460	1	Q9P9L0	Q9P9L0 pyrococcus
38	472.5	16.6	432	14	Q8JZK3	Q8JZK3 uncultured
39	468.5	16.4	457	1	O93647	O93647 thermococcu
40	326.5	11.4	482	2	Q60051	Q60051 thermoactin
41	317	11.1	906	10	Q8LQK4	Q8LQK4 oryza sativ
42	307.5	10.8	423	10	Q8LBS5	Q8LBS5 arabidopsis
43	307.5	10.8	423	10	Q8VZ56	Q8VZ56 arabidopsis
44	307	10.8	826	10	Q9CAR6	Q9CAR6 arabidopsis
45	307	10.8	887	10	Q94A41	Q94A41 arabidopsis

ALIGNMENTS

RESULT 1

Q31193	O31193	PRELIMINARY;	PRT;	549 AA.
AC	O31193;			
DT	01-JAN-1998 (TReMBLrel. 05, Created)			
DT	01-JAN-1998 (TReMBLrel. 05, Last sequence update)			
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)			
DE	Alpha amylase.			
GN	AMI.			
OS	Bacillus stearothermophilus.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.			
OX	NCBI_TaxID=1422;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 31195;			
RA	da Silva A.C.R., Fernandes E., Pueyo M.T.;			
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF032864; AAB86961.1; -			
DR	PIR; A54541; A54541.			
DR	HSP; P06278; 1VJS.			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha amyl cat.			
DR	InterPro; IPR006589; Alp amyl cat sub.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAAMYLASE.			
DR	SMART; SM00642; Amy; 1.			
SQ	SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;			

Query March	99.5%;	Score 2840;	DB 2;	Length 549;
Best Local Similarity	99.6%;	Pred. No. 2.4e-186;		
Matches 513;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	AAPFNGTMQYFEWYLPDDGTLWTKVANEANLSSLGITAIWLPYPAYKTSRSDVGIVY	60	
Db	35	AAPFNGTMQYFEWYLPDDGTLWTKVANEANLSSLGITAIWLPYPAYKTSRSDVGIVY	94	
Qy	61	DLYDLGFEFNQKGTVRTKYTKAQYLOIAHAAGMQYADVDFDHKGADGTWVDVAE	120	

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Db 95 DLYDLGEFNGKGTVRTKYGTAKYQLOAIQAAHAAGMOYADVDFDHKGAGDTEWDAVE 154
QY 121 VNFSDRNOEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
Db 155 VNFSDRNOEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 214
QY 181 IGKAWDEVDTENGNYDLYMYADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240
Db 215 IGKAWDEVDTENGNYDLYMYADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 274
QY 241 FSFPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTYASK 300
Db 275 FSFPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTYASK 334
QY 301 SGGAFDMRTLMTNTLMKDOPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTLMTNTLMKDOPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 394
QY 361 YPCVFGDYGYGIPQVNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGVTEKP 420
Db 395 YPCVFGDYGYGIPQVNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGVTEKP 454
QY 421 GSGLAALITDGGGSKWMYGKQHAGKVFDLTGNSDVTYVINSDDGGEFKVNGGSVSW 480
Db 455 GSGLAALITDGGGSKWMYGKQHAGKVFDLTGNSDVTYVINSDDGGEFKVNGGSVSW 514
QY 481 VPRKTTVSTIARPIITRPTWTFEVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPIITRPTWTFEVRWTEPRLVAMP 549

RESULT 2
Q9KWY6
ID Q9KWY6 PRELIMINARY; PRT; 549 AA.
AC Q9KWY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y17557; CAB93517.1; -.
DR FIR: A54541; A54541.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycoelase; Hydrolase.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CRC64;

Query Match 98.7%; Score 2818; DB 2; Length 549;
Best Local Similarity 99.0%; Pred. No. 7.7e-185;
Matches 510; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPFNGTMQYFEWYLPDDGTILWTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGY 60
Db 35 AAPFNGTMQYFEWYLPDDGTILWTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGY 94
QY 61 DLYDLGEFNGKGTVRTKYGTAKYQLOAIQAAHAAGMOYADVDFDHKGAGDTEWDAVE 120
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Db 95 DLYDLGEFNGKGTVRTKYGTAKYQLOAIQAAHAAGMOYADVDFDHKGAGDTEWDAVE 154
QY 121 VNFSDRNOEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
Db 155 VNFSDRNOEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 214
QY 181 IGKAWDEVDTENGNYDLYMYADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240
Db 215 IGKAWDEVDTENGNYDLYMYADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 274
QY 241 FSFPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTYASK 300
Db 275 FSFPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTYASK 334
QY 301 SGGAFDMRTLMTNTLMKDOPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTLMTNTLMKDOPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 394
QY 361 YPCVFGDYGYGIPQVNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGVTEKP 420
Db 395 YPCVFGDYGYGIPQVNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGVTEKP 454
QY 421 GSGLAALITDGGGSKWMYGKQHAGKVFDLTGNSDVTYVINSDDGGEFKVNGGSVSW 480
Db 455 GSGLAALITDGGGSKWMYGKQHAGKVFDLTGNSDVTYVINSDDGGEFKVNGGSVSW 514
QY 481 VPRKTTVSTIARPIITRPTWTFEVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPIITRPTWTFEVRWTEPRLVAMP 549

RESULT 3
P71034
ID P71034 PRELIMINARY; PRT; 521 AA.
AC P71034;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S.; Chakrabarti T.;
RL "Molecular cloning and expression of the gene encoding for thermostable alpha-amylase of a thermophilic bacterial isolate."; Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;

Query Match 93.1%; Score 2658; DB 2; Length 521;
Best Local Similarity 99.2%; Pred. No. 6.6e-174;
Matches 480; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAPFNGTMQYFEWYLPDDGTILWTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGY 60
Db 35 AAPFNGTMQYFEWYLPDDGTILWTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGY 94
QY 61 DLYDLGEFNGKGTVRTKYGTAKYQLOAIQAAHAAGMOYADVDFDHKGAGDTEWDAVE 120
|||||
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Db 37 NGTWMQYFEWHLPLNDGNHNRRLRDDAANLKSIGITAVWIPPAWKGTSQNDVGYGAYDLVD 96  
QY 65 LGFENQKGTVRTKYGKTAQYLOAQIAHAAGMQUYADVDFHKGAGDGTWVDVAVENPS 124  
Db 97 LGFENQKGTVRTKYGKTRSQLQCAVTSLSKNNGIQVYGVGVMMHKGAGDGTWVNAVENRS 156  
QY 125 DRNQEISGTGTYOIAWTKEFDPGRGNTYSSFKRWYHFDGVUDWDSRKL-SRIYKFRIGK 183  
Db 157 NRNQEISGEYIEATWKEFDPGRGNTSNFKNRWYHFDGTDQSQRLQNKIYKFRGTGK 216  
QY 184 AWDDEVDTENGNDYLMYADLMDHPEVVTYELKKNWGWYVNTTINDGFRDLDAVHKHIFSF 243  
Db 217 AWDDEVDIENGNDYLMYADLMDHPEVINELRNGWYVNTLMDGFRDLDAVHKHIIYS 276  
QY 244 FPDMLSVYRSOTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFFYTASKSGG 303  
Db 277 TRDWLTHVRNTTGKPMFAVAFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLYNASGG 336  
QY 304 AFDMRTLMTWLMKDQPTLATVFDNHDTEPGQALQSWVDWPFKPLAYAFILTRQEGYPC 363  
Db 337 YFDMRNLINGSVQKPHIHAVTFVDNHDSDQGEALSFVQSWFKPLAYALILTRQEGYPS 396  
QY 364 VFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKPGSG 423  
Db 397 VFYGDYGIPTGHPVSMKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGSSHENSG 456  
QY 424 LAALITDPGSGKMYGKQHAGKVFYDLTGNRSDDTVTINSDDGMBGFKVNGSGSVWV 481  
Db 457 LATIMSDPGGKMYGKQHAGKQVWRDITGNRSDDTVTINADGNGFTVNGGAVSVWV 514

RESULT 6  
ID Q9AQ54 PRELIMINARY; PRT; 533 AA.  
AC Q9AQ54;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Alpha-amylase.  
OS Bacillus megaterium.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,  
RA Park K.-H.;  
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium  
KSM B-404."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF220440; AAK00598.1; -.  
DR HSSP; P06278; 1VJS.  
DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha amyl cat.  
DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR SMART; SM00642; Amy; 1.  
SQ SEQUENCE 533 AA; 60557 MW; 789CBCEG6A19C7DDE CRC64;

Query Match 64.5%; Score 1841.5; DB 2; Length 533;  
Best Local Similarity 65.8%; Pred. No. 5.9e-118;  
Matches 317; Conservative 70; Mismatches 92; Indels 3; Gaps 1;  
QY 5 NGTWMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSRSDVGVGVYDLVD 64  
Db 52 NGTLMQYFEWYFNDGNHNRRLTDAENLAQKITSWIPPAKYGTTQNDVGVGAYDLVD 111  
QY 65 LGFENQKGTVRTKYGKTAQYLOAQIAHAAGMQUYADVDFHKGAGDGTWVDVAVENPS 124  
Db 112 LGFENQKGTVRTKYGKTAQYKLSAIDALHKKGNIDVYGDVMMHKGAGDYTTTAVEDVPS 171  
QY 125 DRNQEISGTGTYOIAWTKEFDPGRGNTYSSFKRWYHFDGVUDWDSRKLRIYKFRIGKA 184

Db 172 NRNVESGDYIEISAWTGFNFPGRGDSYSNFKWYHFDGTDWDEGRKLNRIYKFRIGKA 231  
QY 185 WDEVDTENGNDYLMYADLMDHPEVVTYELKKNWGWYVNTTINDGFRDLDAVHKHIFSF 244  
Db 232 WDEVSSENGNDYLMYADLDFDPDVANEMKKGWYANELNLDGFRDLDAVHKHIDHEYL 291  
QY 245 FPDMLSVYRSOTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFFYTASKSGG 304  
Db 292 RDWNVHVRQOTGKEMFAVABYMQNDIQTLNNYLAKVNYNQSVFDPALHYNFHVASKNGN 351  
QY 305 FDMRTLMTWLMKDQPTLATVFDNHDTEPGQALQSWVDWPFKPLAYAFILTRQEGYPCV 364  
Db 352 YDMRNLTKGPMFAVANHPTLATVLENHDSQPGSLESVSWFKPLAYAFILTRAGYPSV 411  
QY 365 FYGDYGI---POYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKPG 421  
Db 412 FYGDYGTGKNSNYEIPALKDKIDPILTARKVAYGTQDYDFDPDVGWTRGGDSVHAN 471  
QY 422 SGALALITDPGSGKMYGKQHAGKVFYDLTGNRSDDTVTINSDDGMBGFKVNGSGSVWV 481  
Db 472 SGLATLISDPGKAWMDVGKNAGBIWYDITGNQNTVTINKDQGWQFQVSGSVSIYV 531  
QY 482 PR 483  
Db 532 QR 533

RESULT 7  
ID Q9QR78 PRELIMINARY; PRT; 519 AA.  
AC Q9QR78;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Raw starch digesting amylase precursor.  
OS Cytophaga sp.  
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;  
OC Flexibacteriaceae; Cytophaga.  
OX NCBI\_TaxID=29535;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jeang C.J., Chen L.S., Chen M.Y.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF067653; AAF00567.1; -.  
DR HSSP; P06278; 1VJS.  
DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha amyl cat.  
DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
DR Pfam; PF00128; alpha-amylase; 1.  
DR PRINTS; PR00110; ALPHAAMYLASE.  
DR SMART; SM00642; Amy; 1.  
KW Signal.  
FT SIGNAL 1 57 POTENTIAL.  
FT CHAIN 58 519 RAW STARCH DIGESTING AMYLASE.  
SQ SEQUENCE 519 AA; 58337 MW; 3E6B88A4DF98B163 CRC64;

Query Match 64.4%; Score 1837.5; DB 2; Length 519;  
Best Local Similarity 67.4%; Pred. No. 1.1e-117;  
Matches 326; Conservative 57; Mismatches 98; Indels 3; Gaps 1;  
QY 1 AAFPNGTWMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSRSDVGVYV 60  
Db 34 AAATNGTWMQYFEWYFNDGQNNRLTDPALVSSVGITAVWTPPAYKGTQADVGYGY 93  
QY 61 DLYDLGEFNQKGTVRTKYGKTAQYLOAQIAHAAGMQUYADVDFHKGAGDGTWVDVAV 120  
Db 94 DLYDLGEFNQKGTVRTKYGKTELKSAVNTLHNSNGIQVYGDVMMHKGADYTNVTAVE 153  
QY 121 VNPSRNOEISGTGTYOIAWTKEFDPGRGNTYSSFKRWYHFDGVUDWDSRKLRIYKFRG 180  
Db 154 VNPSRNOETSGEYNIQAWTGFNFPGRGTTYSNFKWQHPFDGTDWDSRSLRIKFRG 213

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Qy 181 IGKAWDEVDPTNGNYDYLAMADLMDHPVETTELKNGKMYVNTTIDGFRDLDAVKHIK 240
Db 214 TGRAWDWEVSSENGNYDYLAMADLMDHPVETTELKNGKMYVNTTIDGFRDLDAVKHIK 273
Qy 241 FSPFPDMLSVRSOTGKPLFTVGEYWSYDINKLHNYITKTGDTMSLFDAPLHNFYTASK 300
Db 274 FSLFKDWVNARAATGKEMFTVGEYQNDLGLALNLYLAKVYNQSLFDAPLHNFYAAST 333
Qy 301 SGGAFTMTLNTLMTKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 334 GGGYDNRNLTNLTVASNPKATVLVENHDTQGSLESTVQWFKPLAYAFILTRSGG 393
Qy 361 YPCVFGDYD---GIPQYNIPSLKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGT 417
Db 394 YPSVFGDMYGTGTTTRETIPALSKIEPLLKARKDYAYGTQHDYLDHSDIIGWTRREGT 453
Qy 418 EKPSGLAALITDPPGSGKMYVQKQAGKVFYDLTGNSRDTVTINSDGWGEFKNGGVS 477
Db 454 TKAKSGLATVITDPPGSGKMYVGTNSAGEIWTYDLTGRTDKITIGSDGYATFPVNGSV 513
Qy 478 SVWV 481
Db 514 SVWV 517

RESULT 8
Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glucan 1,4-alpha-maltohexosidase (EC 3.2.1.98).
GN BC3482.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Coltanova E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AE017009; AAP10417.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami_cat.
DR InterPro; IPR006589; Alp_ami_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BF9FF6 CRC64;

Query Match 64.1%; Score 1829.5; DB 16; Length 513;
Best Local Similarity 65.6%; Pred. No. 3.7e-117;
Matches 315; Conservative 70; Mismatches 92; Indels 3; Gaps 1;

Qy 5 NGTMQYFEWYLPDDGTLTWTKEANLSSLGITLWLPAYKTSRSDVGYGYDLYD 64
Db 32 NGTMQYFEWYLPDDGTLTWTKEANLSSLGITLWLPAYKTSRSDVGYGYDLYD 91

Qy 65 LGFEFNQKGTVRTKYGTAKYQLQAIQAAHAAGMQUYADVDFHKGADGTWDAVEVNP 124
Db 92 LGFEFNQKGTVRTKYGTAKYQLQAIQAAHAAGMQUYADVDFHKGADGTWDAVEVNP 151
Qy 125 DRNQEISGTQIQAWTKFDPGRGNYSFVKRWTHFGVDGWDSERKLSRIYKFRGIGA 184
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Db 152 NRNEVSGDYEISAWTGFNPPGRGDSYSNFKWYHFDGTDWDEGRKLNRIYKFRGIGA 211
Qy 185 WDEVEVTENGNYDYLAMADLMDHPVETTELKNGKMYVNTTIDGFRDLDAVKHIKESFF 244
Db 212 WDEVEVSSENGNYDYLAMADLMDHPVETTELKNGKMYVNTTIDGFRDLDAVKHIKESFF 271
Qy 245 PDMLSVRSOTGKPLFTVGEYWSYDINKLHNYITKTGDTMSLFDAPLHNFYTASKSGGA 304
Db 272 RDMVNHVRQOTGKEMFTVGEYQNDLGLALNLYLAKVYNQSLFDAPLHNFYAASTGNGN 331
Qy 305 FDMRTLMTLNTLMTKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEGYPCV 364
Db 332 YDMRNILKGVVANHPTLAVTLVENHDSQGSLESTVQWFKPLAYAFILTRQEGYPSV 391
Qy 365 FYGDTYGI---POYNIPSLKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGTKEPG 421
Db 392 FYGDTYGTGKSNVPEIPALCKIDPILTARKNFAYGTQHDYLDHSDIIGWTRREGTKEPG 451
Qy 422 SGLAALITDPPGSGKMYVQKQAGKVFYDLTGNSRDTVTINSDGWGEFKNGGVSVMV 481
Db 452 SGLATLISDGGGAKWMDVGNKNAVWYDITGNTQNTVTINKDQWQFQVSGSVSIYV 511

RESULT 9
Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AWS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niemman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaitte J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami_cat.
DR InterPro; IPR006589; Alp_ami_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 64.0%; Score 1827.5; DB 16; Length 513;
Best Local Similarity 65.8%; Pred. No. 5.1e-117;
Matches 316; Conservative 69; Mismatches 92; Indels 3; Gaps 1;

Qy 5 NGTMQYFEWYLPDDGTLTWTKEANLSSLGITLWLPAYKTSRSDVGYGYDLYD 64
Db 32 NGTMQYFEWYLPDDGTLTWTKEANLSSLGITLWLPAYKTSRSDVGYGYDLYD 91

Qy 65 LGFEFNQKGTVRTKYGTAKYQLQAIQAAHAAGMQUYADVDFHKGADGTWDAVEVNP 124
Db 92 LGFEFNQKGTVRTKYGTAKYQLQAIQAAHAAGMQUYADVDFHKGADGTWDAVEVNP 151
Qy 125 DRNQEISGTQIQAWTKFDPGRGNYSFVKRWTHFGVDGWDSERKLSRIYKFRGIGA 184
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Db 92 LGFEFQKGTVRTKGTGAQLKSALEALHKQIDVIGDVMNKGADYTETVTAVEVDNRN 151
Qy 125 DRNOEISGTYQIOWTKTFFPGRGNTYSSFKRWYHFDGVDMSRKLRIYKFRGIGKA 184
Db 152 NRNVESGDIYSIWSATGPNFGRGNTYSNFKWKYHFDGTDGDKLNRIYKFRGIGKA 211
Qy 185 WDWEVDTEGNYDYLMDADLMDHPEVVTTELKNNKWKYVNTTNDGFRDLDAVKHIFKSF 244
Db 212 WDWEVSSGNGYDYLMDADLDFDHPVANEMKNGTWTYANELNDGFRDLDAVKHIDHEYL 271
Qy 245 PDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYIKTDGTSMSLFDAPLHNKFTASKSGGA 304
Db 272 RDWNHVRQQTGKEMFTVAETWQNDIOTLNNYLAKVNYNSQVFDAPLHNFYASKNGN 331
Qy 305 FDMRTLMTNTLMKDOPTLAVTFVDNHDTEPGALQSWVDWPFKPLAYAFILTRQEGYPCV 364
Db 332 YDMENILNGTVMQNHAPALAVTLVENHDSQPGQSLESVSVFWRKPLAYAFILTRAEYPSV 391
Qy 365 FYGDIYGI---PQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGTEKPG 421
Db 392 FYGDIYGTSGNSSYEIPALKDKIDPILTARKNFAYGRTQDYLDPDVGWTRREGDSVHAN 451
Qy 422 SGLAALITDGPCKGSKMYVQKHAGKYFYDLTGNRSDDTVTINSNGWGEFVKNGSGSVWV 481
Db 452 SGLATLISDGPCKGSKMDVQKNAAGYVHDMTGNTQNTVINKDQNGQFHVSGGSVIYV 511

RESULT 10
Q87HG6 PRELIMINARY; PRT; 507 AA.
AC Q87HG6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN VFA0999.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Vibrio.
NCBI_TaxID=670;
[1]
SEQUENCE FROM N.A.
RC STRAIN=RMID 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62342.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
KW Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

Query Match 59.6%; Score 1700; DB 16; Length 507;
Best Local Similarity 63.1%; Pred. No. 2,7e-108;
Matches 305; Conservative 66; Mismatches 102; Indels 10; Gaps 6;

Qy 5 NGTMMQYFEWLPDDGTTLTKVANEANNLSLIGITALWLPAYKGTSRSDVGVYDLY 63
Db 26 NGTMMQYFHHVYVNDGALMTQVESNPALAEAGFTALWLPAYKAGGNDVGYDLY 85
Qy 64 DLGEFNQKGTVRTKGTGAQYLOAIQAHAAGQVYADVVDVFDHKGADGTETWDAVENP 123
Db 86 DLGEFDQKGSVRTKGTGAQYISAINAAHNNIYIGYDVVFNHGGADGKSWDTKRVDW 145
Qy 124 SDRNQISGTYQIOWTKTFFPGRGNTYSSFKRWYHFDGVDMSRKLRIYKFRGIGK 183

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Db 146 DNRNIEL-GDKWIEAWVEFNFPGRNDKYSNFHHTWTHFDGVDWDDAGKEKAIKFKGEGK 204
Qy 184 AWDWEVDTEGNYDYLMDADLMDHPEVVTTELKNNKWKYVNTTNDGFRDLDAVKHIFKSF 243
Db 205 AWDWEVSSEKNGYDYLMDADLMDHPEVVKQELKDWGEWYINMTGVDGFRMDAVKHICYQ 264
Qy 244 FPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYIKTDGTSMSLFDAPLHNKFTASKSGG 303
Db 265 LQEWIDHLRWKTKELFTVGEYWNVDVNLHNPITKTSMSLFDAPLHNFYASKSGG 324
Qy 304 AFDMRTLMTNTLMKDOPTLAVTFVDNHDTEPGALQSWVDWPFKPLAYAFILTRQEGYPC 363
Db 325 NYDMRQIMNGTLMKDNPKVKAIVLNVHNDTQPLQALSTVDWMPKPLAYAFILTRQEGYPS 384
Qy 364 VFYGDYGIYGPQ----YNIPSLK-SKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGTE 418
Db 385 VFADYIYGAQYSDKGNINNAKVPYIEELVTLKKEYAYGKNSYLDHNDVIGWTRREGDAE 444
Qy 419 KPGSGLAALITDGPCKGSKMYVQKHAGKYFYDLTGNRSDDTVTINSNGWGEFVKNGSGVS 478
Db 445 HPNS-MAVIMSDGPGCKGKMYTGKPSR--YVDKLGIRTEEVWTDANGWAEFPVNGSGVS 501
Qy 479 VWV 481
Db 502 VWV 504

RESULT 11
Q93I48 PRELIMINARY; PRT; 501 AA.
AC Q93I48;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYK38.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=129736;
[1]
SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayashi Y.;
RT "Isolation of a new Bacillus alpha-amylase."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051102; BAB71820.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

Query Match 56.7%; Score 1618; DB 2; Length 501;
Best Local Similarity 59.3%; Pred. No. 1.1e-102;
Matches 283; Conservative 80; Mismatches 112; Indels 2; Gaps 1;

Qy 5 NGTMMQYFEWLPDDGTTLTKVANEANNLSLIGITALWLPAYKGTSRSDVGVYDLY 64
Db 25 NGTMMQYFEWHLNDCQHNRLHDDAALSDAGITAITWIPPAKGNQSDAVGVYDLY 84
Qy 65 LGFEFNQKGTVRTKGTGAQYLOAIQAHAAGQVYADVVDVFDHKGADGTETWDAVENP 124
Db 85 LGFEFNQKGTVRTKGTGAQLERAIGLSKNSDINVDVVMNHNKMGADFTAEVQAVQVNET 144
Qy 125 DRNOEISGTYQIOWTKTFFPGRGNTYSSFKRWYHFDGVDMSRKLRIYKFRGIGKA 184
Db 145 NRWQDISGATYITDAGTGFDFSGRNNAYSDFKRWYHFNHGGADGQRYQENHIFRANTN-- 202
Qy 185 WDWEVDTEGNYDYLMDADLMDHPEVVTTELKNNKWKYVNTTNDGFRDLDAVKHIFKSF 244
Db 203 WNRVDEENGNDYLLGNSIDFSHPEVQDELKQWSWTFDELDGRLDAIKHIFPFWT 262
Qy 245 PDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYIKTDGTSMSLFDAPLHNKFTASKSGGA 304

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Db 263 SDWVRHQRNEADQDLFVVGWYKDDVGCALFYLDENWMSLFDVPLNRYFYRASQOQGS 322
Qy 305 FDMRTLMTNTLMKDOPTLAVTFVDNHDTEPQALQSWVDWPKFLAYAFILTRQGYPCV 364
Db 323 YDMNIRLGSVEAHFPHAVTFVDNHDTEPQALQSWVDWPKFLAYAFILTRQGYPCV 382
Qy 365 FYGDIYGIPOVNIPLSKIDPLLIARDYAYGTQHDYLDHSDIIGWTRGGTEKPGSGL 424
Db 383 FYGDIYGIPOVNIPLSKIDPLLIARDYAYGTQHDYLDHSDIIGWTRGGTEKPGSGL 442
Qy 425 AALITDGPQSGKMYVQKQAGKVFYDITGNRSTVTNIDGCEFKVNGSGSVVWV 481
Db 443 ATIMNSPGGSKMYVQKQAGKVFYDITGNRSTVTNIDGCEFKVNGSGSVVWV 499

RESULT 12
Q8YUZI PRELIMINARY; PRT; 492 AA.
AC Q8YUZI
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylose.
GN ALR2190.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003588; BAB73889.1; -
DR FRC; AH2079; AH2079.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylose; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
KW Complete proteome.
SQ SEQUENCE 492 AA; 57063 MW; 11B5D6ECP2F18288 CRC64;

Query Match 47.1%; Score 1345.5; DB 16; Length 492;
Best Local Similarity 52.8%; Pred. No. 5e-84;
Matches 261; Conservative 67; Mismatches 147; Indels 19; Gaps 7;

Qy 2 APFNGTMMQYFEWYLPDDGTLTWKVANEANLSSIGITLWLPAYKGTGRS-DVYGQVY 60
Db 2 AQWNGTMMQYFHWYIPNDGNLWSKVEASAPELADAGTAMWLPAYKGFAGSVFVGQVY 61
Qy 61 DLYDLGFEQNGKVTRTKYGTQAQYLOIAQAAHAGMOMYADVDPDRHKGADGTETWDAVE 120
Db 62 DLFDLGFEQNGKVTRTKYGTQAQYLOIAQAAHAGMOMYADVDPDRHKGADGTETWDAVE 121
Qy 121 VNPSSDRNQEISGTYQIAQWTKFDPGRGNTYSSFKRWYHFDGVDWDE--SRKLSRIYKF 178
Db 122 FPQDDRLNPKRGGLODKITYTHNPFGRGKYSNFEWHWHFDDAVDYNEYSNGDSTVYLL 181
Qy 179 RGTGKANDWEVDTEGNGYDLYMADLMDHPVETELKNWGWVNTTNDIGFRLDAVKH 238
Db 182 E--GKNFDDYVALEKGNFAYLMGCDLDFQNEWVGEVITYWGWKCLDITTKVDGFRIDA 239
Qy 239 IKFSFFPDWLSYRASQTKPLFTVGEYWSYDINKLHNYITKTDTGMSLFDAPLHNFYTA 298
Db 240 ISTWFFFWIDALERHAGKOLFWMYGEVYNDINTLLWYVDVAVRGKMSVDFVPLHNFHQA 299
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Qy 299 SKSGAFDMRTLMTNTLMKDOPTLAVTFVDNHDTEPQALQSWVDWPKFLAYAFILTRQ 358
Db 300 SKSGAFDMRTLMTNTLMKDOPTLAVTFVDNHDTEPQALQSWVDWPKFLAYAFILTRQ 359
Qy 359 EGYPCVFGYGYGIP-----QYNI--PSLKSIDPLLIARDYAYGTQHDYLDHSD 407
Db 360 EGYPCVFGYGYGIP-----QYNI--PSLKSIDPLLIARDYAYGTQHDYLDHSD 419
Qy 408 IIGWTRGGTEKPGSGLAALITDGPQSGKMYVQKQAGKVFYDITGNRSTVTNIDGCE 467
Db 420 TIGWTRGGTEKPGSGLAALITDGPQSGKMYVQKQAGKVFYDITGNRSTVTNIDGCE 476
Qy 468 GEFKVGSGSVVWV 481
Db 477 GEFKVGSGSVVWV 490

RESULT 13
Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylose precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RX Xu J., Bjurcell M.K., Himrod J., Deng S., Carmichael L.K.,
RX Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; -
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

Query Match 46.3%; Score 1322.5; DB 16; Length 481;
Best Local Similarity 49.3%; Pred. No. 1.8e-82;
Matches 236; Conservative 89; Mismatches 153; Indels 1; Gaps 1;

Qy 5 NGTMMQYFEWYLPDDGTLTWKVANEANLSSIGITLWLPAYKGTGRSDVYGQVYDLYD 64
Db 3 NGTMMQYFEWYLPDDGTLTWKVANEANLSSIGITLWLPAYKGTGRSDVYGQVYDLYD 62
Qy 65 LGEPNQKGTVRTKYGTQAQYLOIAQAAHAGMOMYADVDPDRHKGADGTETWDAVE 124
Db 63 LGEPNQKGTVRTKYGTQAQYLOIAQAAHAGMOMYADVDPDRHKGADGTETWDAVE 122
Qy 125 DRNQEISGTYQIAQWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRGIGKA 184
Db 123 ERTKALGEPPEIQGTGYSFGRKDKHSDPKFWHWHFSGTGFDDAQKRSVQIQSGKA 182
Qy 185 WDMEDVTENGNDYDLYMADLMDHPVETELKNWGWVNTTNDIGFRLDAVKHIFKFSFF 244
Db 183 WSEGVDSNGYDLYMADLMDHPVETELKNWGWVNTTNDIGFRLDAVKHIFKFSFF 242
Qy 245 PDMLSYRSTQKPLFTVGEYWSYDINKLHNYITKTDTGMSLFDAPLHNFYTA 304
Db 243 AQFLDAVRSERGNDFYAVGEYWDLEALDAYTEAVGHKVNLFDPVPLHNFHQA 302
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Db	63	LGSEFNKGTVRTKYGFKEBLYQAIQALKAQGIQPMADVVLNHHKAAADHREAFQVIEVDPV	122
Qy	125	DRNQEISGTYQIQAWTKFDPGGRGNTYSSFKRWYHFDGVDDWDESRKLSRIYKFRGIGKA	184
Db	123	DRTVEGEPETNGWTSFTDGRQDTYNGFHHWHYFTGTDYDAKRSKGILYLQGNKG	182
Qy	185	WDWE--VDTENGNYDYLMYADLMDHDPVVTTELKNWGKYVNTTNIIDGFRLDAVKHKFS	242
Db	183	WANEELVDNENGNYDYLMYADLDPKFPEVIQNIYDMDWDFMETTGAVAGFRLDAVKHDSF	242
Qy	243	FPFDWLISYRSQTKPLFTTGEYWSYDINKLHNIITKTDTGMSLFDAPLHNKFTTASKSG	302
Db	243	FMENFIRDMKEKYGDPPYVGEFWSNDEKANLDYLEKTEEHFDLVDRLHQNLFEASQAG	302
Qy	303	GAFDMRTLMTNLMKOOPTLAVTVPDVNDHDTFPGQALOSWDPDPKPLAYAFILROEGYP	362
Db	303	ANYDLRGIFTSLVELPKDXAVTVPDVNDHTQRGQALESTVEEWFKPAAIILURQDGLP	362
Qy	363	CVFVGDYVYGTIP-QYNIPSLSKSIDPLLIARDDYAYGTHDYLDSHSDIIGTWREGTEKPG	421
Db	363	CVFVGYIGLGGYQAQDFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWRSGAENQ--	420
Qy	422	SGLAALITDGGGSKWNYVGQKHAGKYVPYDITGNRSDDTITNSDGWGSEFKYNGGVSVMV	481
Db	421	SPITAVLISNDQENSKSMFVGQEWNTQFVDLLGSHQGQVTTIDEGYGGQFPYSARSVSYM-	479
Qy	482	PRKTTVSTI	490
Db	480	----AVNTI	484

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 15.9573 Seconds  
(without alignments)  
1666.155 Million cell updates/sec

Title: US-09-925-576C-6  
Perfect score: 2854  
Sequence: 1 AAPFNGTMMQYFEWYLPDDG.....TRPWTGEFVRWTEPRILVAMP 515

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2854	100.0	515	4	US-09-291-023A-17
2	2854	100.0	515	4	US-09-537-168-8
3	2854	100.0	515	4	US-09-540-715A-17
4	2854	100.0	549	1	US-08-720-899-6
5	2854	100.0	549	1	US-08-459-610-6
6	2854	100.0	549	2	US-08-343-804-6
7	2854	100.0	549	2	US-08-687-399-6
8	2854	100.0	549	2	US-08-600-908A-6
9	2854	100.0	549	3	US-08-683-838A-6
10	2854	100.0	549	4	US-09-636-252A-6
11	2847	99.8	514	3	US-08-182-859-6
12	2847	99.8	514	3	US-08-284-097-8
13	2847	99.8	514	4	US-09-672-459-6
14	2847	99.8	514	4	US-10-186-042-6
15	2812	98.5	515	4	US-09-381-687-7
16	2780	97.4	514	3	US-08-600-656-3
17	2780	97.4	514	3	US-09-170-670-3
18	2780	97.4	514	3	US-09-193-068-3
19	2780	97.4	514	3	US-09-183-412-3
20	2780	97.4	514	3	US-09-354-191A-3
21	2780	97.4	514	4	US-09-290-734-3
22	2780	97.4	514	4	US-09-545-586-3
23	2780	97.4	514	4	US-09-769-864-3
24	2727.5	95.6	548	1	US-08-468-700-37
25	2727.5	95.6	548	1	US-08-645-971-5
26	2727.5	95.6	548	2	US-08-468-220-35
27	2727.5	95.6	548	2	US-08-468-698-35

#### ALIGNMENTS

##### RESULT 1

US-09-291-023A-17  
; Sequence 17, Application US/09291023A

; Patent No. 6309871

; GENERAL INFORMATION:

; APPLICANT: Outtrup, Helle

; APPLICANT: Borchert, Torben

; APPLICANT: Nielsen, Bjarne

; APPLICANT: Nielsen, Vibeke

; APPLICANT: Hoeck, Lisbeth

; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A

; FILE REFERENCE: 5821.010-US

; CURRENT APPLICATION NUMBER: US/09/291,023A

; CURRENT FILING DATE: 1999-04-13

; PRIOR APPLICATION NUMBER: DK 1999 00438

; PRIOR FILING DATE: 1999-03-31

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 17

; TYPE: PRT

; LENGTH: 515

; ORGANISM: Bacillus

US-09-291-023A-17

Query Match 100.0%; Score 2854; DB 4; Length 515;

Best Local Similarity 100.0%; Pred. NO. 5.4e-246;

Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAPFNGTMMQYFEWYLPDDGTLTKVANEANNSSLGITATLWLPAYKGTSRSDVGXGVY 60

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Db 61 DLVDLGEFNGKGTVRTKYGKAOYLQAIQAHAAGMOYADVVDHKGAGDGTIEWDAVE 120

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Db 181 IGKAWDWEVTENGNGYDLYMAYDLMDHPVVTTELKNGKQWYNTTINDGFRDLDAVKHK 240

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Db 361 YPCVFYGDYIGIPQYNIPSLKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
Qy 421 GSGLAALITDGPGGSKMVMYVKGQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480  
Db 421 GSGLAALITDGPGGSKMVMYVKGQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480  
Qy 481 VPRKTTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 515  
Db 481 VPRKTTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 515  
RESULT 2  
US-09-537-168-8  
; Sequence 8, Application US/09537168  
; Patent No. 6410295  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Carsten  
; APPLICANT: Jorgensen, Christel T.  
; APPLICANT: Bisgaard-Franzen, Henrik  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Kjaerulff, Soren  
; TITLE OF INVENTION: Alpha-Amylase Variants  
; FILE REFERENCE: 5886.200-US  
; CURRENT APPLICATION NUMBER: US/09/537,168  
; CURRENT FILING DATE: 2000-03-29  
; EARLIER APPLICATION NUMBER: PA 1999 00437  
; EARLIER FILING DATE: 1999-03-30  
; EARLIER APPLICATION NUMBER: 60/127,427  
; EARLIER FILING DATE: 1999-04-01  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 515  
; TYPE: PRT  
; ORGANISM: Bacillus stearothermophilus  
US-09-537-168-8  
Query Match 100.0%; Score 2854; DB 4; Length 515;  
Best Local Similarity 100.0%; Pred. No. 5.4e-246;  
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYY 60  
Db 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYY 60  
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Db 61 DLYDLGEFNQKGTVRTKYGTAKQYLQAIQAAHAAGQVYADVDFDHKGADGTEWDAVE 120  
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; Sequence 17, Application US/09540715A  
; Patent No. 6623948  
; GENERAL INFORMATION:  
; APPLICANT: Outtrup, Helle  
; APPLICANT: Borchert, Torben  
; APPLICANT: Nielsen, Bjarne  
; APPLICANT: Nielsen, Vibeke  
; APPLICANT: Hoeck, Lisbeth  
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Ac  
; FILE REFERENCE: 5821.010-US  
; CURRENT APPLICATION NUMBER: US/09/540,715A  
; CURRENT FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/291,023  
; PRIOR FILING DATE: 2001-08-14  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 515  
; TYPE: PRT  
; ORGANISM: Bacillus  
US-09-540-715A-17  
Query Match 100.0%; Score 2854; DB 4; Length 515;  
Best Local Similarity 100.0%; Pred. No. 5.4e-246;  
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYY 60  
Db 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYY 60  
Qy 61 DLYDLGEFNQKGTVRTKYGTAKQYLQAIQAAHAAGQVYADVDFDHKGADGTEWDAVE 120  
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Qy 121 VNPSDRNQEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180  
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Qy 181 IGKAWDEVDTEGNGYDYLMYADLMDHDPVVTTELKNWGWYNTNIDGFRDLDAVKHK 240  
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Db 361 YPCVFYGDYIGIPQYNIPSLKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
Qy 421 GSGLAALITDGPGGSKMVMYVKGQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480  
Db 421 GSGLAALITDGPGGSKMVMYVKGQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480  
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Db 395 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 454
Qy 421 GSGLAALITDGGGSKWMYVGKHAGKVFYDLTGNSRSDTVTINS DGMGEPKVGSGSVW 480
Db 455 GSGLAALITDGGGSKWMYVGKHAGKVFYDLTGNSRSDTVTINS DGMGEPKVGSGSVW 514
Qy 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 549

RESULT 6
US-08-343-804-6
; Sequence 6, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESSES:
; ADDRESS: No. 5830837c No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 549 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-343-804-6
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Query Match 100.0%; Score 2854; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 6e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 215 IGKAWDEVDTEGNYDYLMDHDPVVTTELKNGWKWYNTTNDGFRDLDAVKHIK 274
Qy 241 FSPFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTASK 300
Db 275 FSPFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTASK 334
Qy 301 SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWPKLAYAFILTRQEG 360
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Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 395 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 454
Qy 421 GSGLAALITDGGGSKWMYVGKHAGKVFYDLTGNSRSDTVTINS DGMGEPKVGSGSVW 480
Db 455 GSGLAALITDGGGSKWMYVGKHAGKVFYDLTGNSRSDTVTINS DGMGEPKVGSGSVW 514
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Db 515 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 549

RESULT 7
US-08-687-399-6
; Sequence 6, Application US/08687399
; Patent No. 5928381
; GENERAL INFORMATION:
; APPLICANT: Toft, Annette H.
; APPLICANT: Marcher, Dorte
; APPLICANT: Pedersen, Hanne E.
; APPLICANT: Nilsson, Thomas E.
; TITLE OF INVENTION: A Combined Desizing and Bleaching
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESS: No. 5928381c No. 5928381disk of No. 5928381th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,399
; FILING DATE:
; CLASSIFICATION: 008
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
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; REFERENCE/DOCKET NUMBER: 4127.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 549 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-687-399-6

Query Match 100.0%; Score 2854; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 6e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 35 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSSLGITALTALWLPAYKGTSRSDVG YVY 94

QY 61 DLYDLGEFNGKGTVRTKYTKAQYLOAIQAHAAGMOVYADVDFDHKGGADGTWVD AVE 120
DB 95 DLYDLGEFNGKGTVRTKYTKAQYLOAIQAHAAGMOVYADVDFDHKGGADGTWVD AVE 154

QY 121 VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 180
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QY 181 IGKAWDEVDTEGNDYDLYMYADLDMDHPEVVTTELKNWGWYNTTINIDGFRDLDAVKHIK 240
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QY 241 FSFPFDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDPALHNKFTYASK 300
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QY 421 GSGLAALITDGPCKGKMYVKGQHAGKVYFDLTGNRSDDTVTINSDGWGEFKVNGGSVSW 480
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QY 481 VPRKTTVSTIARPIITRPWTGFEFVRWTEPRLVAMP 515
DB 515 VPRKTTVSTIARPIITRPWTGFEFVRWTEPRLVAMP 549

RESULT 9
US-08-600-908A-6
; Sequence 6, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: "-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 549 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-600-908A-6

Query Match 100.0%; Score 2854; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 6e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSSLGITALTALWLPAYKGTSRSDVG YVY 60
DB 35 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSSLGITALTALWLPAYKGTSRSDVG YVY 94

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DB 95 DLYDLGEFNGKGTVRTKYTKAQYLOAIQAHAAGMOVYADVDFDHKGGADGTWVD AVE 154

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QY 181 IGKAWDEVDTEGNDYDLYMYADLDMDHPEVVTTELKNWGWYNTTINIDGFRDLDAVKHIK 240
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QY 241 FSFPFDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDPALHNKFTYASK 300
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QY 301 SGGAADMRTLTMTLTKMDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360
DB 335 SGGAADMRTLTMTLTKMDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 394

QY 361 YPCVFYDYYGIPQYNIPLSKSDIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGGTEKP 420
DB 395 YPCVFYDYYGIPQYNIPLSKSDIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGGTEKP 454

QY 421 GSGLAALITDGPCKGKMYVKGQHAGKVYFDLTGNRSDDTVTINSDGWGEFKVNGGSVSW 480
DB 455 GSGLAALITDGPCKGKMYVKGQHAGKVYFDLTGNRSDDTVTINSDGWGEFKVNGGSVSW 514

QY 481 VPRKTTVSTIARPIITRPWTGFEFVRWTEPRLVAMP 515
DB 515 VPRKTTVSTIARPIITRPWTGFEFVRWTEPRLVAMP 549

RESULT 9
US-08-683-838A-6
; Sequence 6, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: "-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.  
STREET: 405 Lexington Avenue, 64th floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/683,838A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/600,908  
FILING DATE: 13-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 4394.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 549 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-683-838A-6

Query Match 100.0%; Score 2854; DB 3; Length 549;  
Best Local Similarity 100.0%; Pred. No. 6e-246;  
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSLIGITALWLPAYKGTSRSDVG 60  
DB 35 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSLIGITALWLPAYKGTSRSDVG 94  
QY 61 DLYDLGEFNGKGTVRTKYGTAKQYLQAIQAHAAGMQVYADVDFDHKGADGTEWDAVE 120  
DB 95 DLYDLGEFNGKGTVRTKYGTAKQYLQAIQAHAAGMQVYADVDFDHKGADGTEWDAVE 154  
QY 121 VNPSDRNQEISGTYQIQAWTKFDPGKNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
DB 155 VNPSDRNQEISGTYQIQAWTKFDPGKNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214  
QY 181 IGKAWDEVDVTENGNDYDLYMYADLDMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240  
DB 215 IGKAWDEVDVTENGNDYDLYMYADLDMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 274  
QY 241 FSFPFOWLSVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300  
DB 275 FSFPFOWLSVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 334  
QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360  
DB 335 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 394  
QY 361 YPCVFYGDYIGIPQYNIPLSKIDPLLIARRDYAYGTOHDYLDHSDIIGWTREGGTEKP 420  
DB 395 YPCVFYGDYIGIPQYNIPLSKIDPLLIARRDYAYGTOHDYLDHSDIIGWTREGGTEKP 454  
QY 421 GSGLAALITDGPCKGKMWYVKGQHAGKVFDYLTGNRSDVTITNSDGMGKFKVNGGVSVM 480  
DB 455 GSGLAALITDGPCKGKMWYVKGQHAGKVFDYLTGNRSDVTITNSDGMGKFKVNGGVSVM 514  
QY 481 VPRKTTVSTIARPIITRPWTGFEVWTEPRLVAMP 515  
DB 515 VPRKTTVSTIARPIITRPWTGFEVWTEPRLVAMP 549

RESULT 10  
US-09-636-252A-6  
; Sequence 6, Application US/09636252A  
; Patent No. 6440716  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Bisgard-Frantzen, Henrik  
; APPLICANT: Borchert, Torben Vedel  
; TITLE OF INVENTION: Alpha-Amylase Mutants  
; FILE REFERENCE: 0776/1F216-US2  
; CURRENT APPLICATION NUMBER: US/09/636,252A  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 08/683,838  
; PRIOR FILING DATE: 1996-07-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; TYPE: PRT  
; LENGTH: 549  
; ORGANISM: B. stearothermophilus  
US-09-636-252A-6

Query Match 100.0%; Score 2854; DB 4; Length 549;  
Best Local Similarity 100.0%; Pred. No. 6e-246;  
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSLIGITALWLPAYKGTSRSDVG 60  
DB 35 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSLIGITALWLPAYKGTSRSDVG 94  
QY 61 DLYDLGEFNGKGTVRTKYGTAKQYLQAIQAHAAGMQVYADVDFDHKGADGTEWDAVE 120  
DB 95 DLYDLGEFNGKGTVRTKYGTAKQYLQAIQAHAAGMQVYADVDFDHKGADGTEWDAVE 154  
QY 121 VNPSDRNQEISGTYQIQAWTKFDPGKNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
DB 155 VNPSDRNQEISGTYQIQAWTKFDPGKNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214  
QY 181 IGKAWDEVDVTENGNDYDLYMYADLDMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240  
DB 215 IGKAWDEVDVTENGNDYDLYMYADLDMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 274  
QY 241 FSFPFOWLSVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300  
DB 275 FSFPFOWLSVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 334  
QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360  
DB 335 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 394  
QY 361 YPCVFYGDYIGIPQYNIPLSKIDPLLIARRDYAYGTOHDYLDHSDIIGWTREGGTEKP 420  
DB 395 YPCVFYGDYIGIPQYNIPLSKIDPLLIARRDYAYGTOHDYLDHSDIIGWTREGGTEKP 454  
QY 421 GSGLAALITDGPCKGKMWYVKGQHAGKVFDYLTGNRSDVTITNSDGMGKFKVNGGVSVM 480  
DB 455 GSGLAALITDGPCKGKMWYVKGQHAGKVFDYLTGNRSDVTITNSDGMGKFKVNGGVSVM 514  
QY 481 VPRKTTVSTIARPIITRPWTGFEVWTEPRLVAMP 515  
DB 515 VPRKTTVSTIARPIITRPWTGFEVWTEPRLVAMP 549

RESULT 11  
US-09-182-859-6  
; Sequence 6, Application US/09182859  
; Patent No. 6143708  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Borchert, Torben  
; APPLICANT: Bisgard-Frantzen, Henrik  
; TITLE OF INVENTION: Alpha-Amylase Mutants



FILE REFERENCE: 4796.204-US  
CURRENT APPLICATION NUMBER: US/09/182.859  
EARLIER FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: 0515/96  
EARLIER FILING DATE: 1996-04-30  
EARLIER APPLICATION NUMBER: 0712/96  
EARLIER FILING DATE: 1996-06-28  
EARLIER APPLICATION NUMBER: 0775/96  
EARLIER FILING DATE: 1996-07-11  
EARLIER APPLICATION NUMBER: 1263/96  
EARLIER FILING DATE: 1996-11-08  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 514  
TYPE: PRT  
ORGANISM: Bacillus stearothermophilus  
US-09-182-859-6

Query Match 99.8%; Score 2847; DB 3; Length 514;  
Best Local Similarity 100.0%; Pred. No. 2.3e-245;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSSLGITLWLPAYKTSRSDVGYGVY 60  
Db 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSSLGITLWLPAYKTSRSDVGYGVY 60  
Qy 61 DLYDLGFEFNQKGTVRTKYGTAKYQALQIAAHAGMOVYADVDFDHKGADGTEWDAVE 120  
Db 61 DLYDLGFEFNQKGTVRTKYGTAKYQALQIAAHAGMOVYADVDFDHKGADGTEWDAVE 120  
Qy 121 VNPSDRNOEISGTYQIQAWTKFDPGCGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
Db 121 VNPSDRNOEISGTYQIQAWTKFDPGCGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
Qy 181 IGKAWDEVDTEGNGYDYLADMDHPEVVTTELKNGKMYVNTNIDGFRDLDAVKHIK 240  
Db 181 IGKAWDEVDTEGNGYDYLADMDHPEVVTTELKNGKMYVNTNIDGFRDLDAVKHIK 240  
Qy 241 FSPFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFADPLHNKFTYASK 300  
Db 241 FSPFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFADPLHNKFTYASK 300  
Qy 301 SGGAFFMRLTMTLTKMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
Db 301 SGGAFFMRLTMTLTKMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
Qy 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
Db 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
Qy 421 GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNRSDTVTINS DGGEFKVNGGSVSW 480  
Db 421 GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNRSDTVTINS DGGEFKVNGGSVSW 480  
Qy 481 VPRKTTVSTIARPTTRPWTGFEFVRWTEPRLVAV 514  
Db 481 VPRKTTVSTIARPTTRPWTGFEFVRWTEPRLVAV 514

RESULT 12  
US-09-264-097-8  
Sequence 8, Application US/09264097  
Patent No. 6287826  
GENERAL INFORMATION:  
APPLICANT: Hendriksen, Hanne Vang  
APPLICANT: No. 6287826man, Barrie Edmund  
TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup  
TITLE OF INVENTION: From Starch  
FILE REFERENCE: 5278.200-US  
CURRENT APPLICATION NUMBER: US/09/264.097  
CURRENT FILING DATE: 1999-03-08  
EARLIER APPLICATION NUMBER: PA 0321/98

EARLIER FILING DATE: 1998-03-09  
EARLIER APPLICATION NUMBER: 60/079,209  
EARLIER FILING DATE: 1998-03-24  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 514  
TYPE: PRT  
ORGANISM: Bacillus  
US-09-264-097-8  
Query Match 99.8%; Score 2847; DB 3; Length 514;  
Best Local Similarity 100.0%; Pred. No. 2.3e-245;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSSLGITLWLPAYKTSRSDVGYGVY 60  
Db 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSSLGITLWLPAYKTSRSDVGYGVY 60  
Qy 61 DLYDLGFEFNQKGTVRTKYGTAKYQALQIAAHAGMOVYADVDFDHKGADGTEWDAVE 120  
Db 61 DLYDLGFEFNQKGTVRTKYGTAKYQALQIAAHAGMOVYADVDFDHKGADGTEWDAVE 120  
Qy 121 VNPSDRNOEISGTYQIQAWTKFDPGCGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
Db 121 VNPSDRNOEISGTYQIQAWTKFDPGCGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180  
Qy 181 IGKAWDEVDTEGNGYDYLADMDHPEVVTTELKNGKMYVNTNIDGFRDLDAVKHIK 240  
Db 181 IGKAWDEVDTEGNGYDYLADMDHPEVVTTELKNGKMYVNTNIDGFRDLDAVKHIK 240  
Qy 241 FSPFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFADPLHNKFTYASK 300  
Db 241 FSPFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFADPLHNKFTYASK 300  
Qy 301 SGGAFFMRLTMTLTKMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
Db 301 SGGAFFMRLTMTLTKMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360  
Qy 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
Db 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  
Qy 421 GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNRSDTVTINS DGGEFKVNGGSVSW 480  
Db 421 GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNRSDTVTINS DGGEFKVNGGSVSW 480  
Qy 481 VPRKTTVSTIARPTTRPWTGFEFVRWTEPRLVAV 514  
Db 481 VPRKTTVSTIARPTTRPWTGFEFVRWTEPRLVAV 514

RESULT 13  
US-09-672-459-6  
Sequence 6, Application US/09672459  
Patent No. 6436888  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Borchert, Torben  
APPLICANT: Bisgaard-Frantzen, Henrik  
TITLE OF INVENTION: Alpha-Amylase Mutants  
FILE REFERENCE: 4796.204-US  
CURRENT APPLICATION NUMBER: US/09/672.459  
CURRENT FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: 09/182,859  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 0515/96  
PRIOR FILING DATE: 1996-04-30  
PRIOR APPLICATION NUMBER: 0712/96  
PRIOR FILING DATE: 1996-06-28  
PRIOR APPLICATION NUMBER: 0775/96  
PRIOR FILING DATE: 1996-07-11  
PRIOR APPLICATION NUMBER: 1263/96

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; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-672-459-6

Query Match          99.8%; Score 2847; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPNGTMMQYFEWYLPDDGTLTKVANEANNNSSLGITALLWLPAYKGTSRSDVGYY 60
DB 1 AAPNGTMMQYFEWYLPDDGTLTKVANEANNNSSLGITALLWLPAYKGTSRSDVGYY 60

QY 61 DLYDLGEFNQKGTVRTKYGTAKYQLOAIQAHAAGMQVYADVVDHKGADGTWDAVE 120
DB 61 DLYDLGEFNQKGTVRTKYGTAKYQLOAIQAHAAGMQVYADVVDHKGADGTWDAVE 120

QY 121 VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
DB 121 VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180

QY 181 IGKAWDEVDTEGNYDYLAMYADLMDHPVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240
DB 181 IGKAWDEVDTEGNYDYLAMYADLMDHPVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240

QY 241 FSFPDWLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300
DB 241 FSFPDWLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300

QY 301 SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWPKLAYAFILTRQEG 360
DB 301 SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWPKLAYAFILTRQEG 360

QY 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
DB 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDPPGSGKMMYVKGQHAGKVFDYLTGNRSDTVTINSQGWGEFKVNGGSVSW 480
DB 421 GSGLAALITDPPGSGKMMYVKGQHAGKVFDYLTGNRSDTVTINSQGWGEFKVNGGSVSW 480

QY 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRVAV 514
DB 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRVAV 514

RESULT 14
US-10-186-042-6
; Sequence 6, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Prantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186, 042
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672, 459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182, 859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96

; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-10-186-042-6

Query Match          99.8%; Score 2847; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPNGTMMQYFEWYLPDDGTLTKVANEANNNSSLGITALLWLPAYKGTSRSDVGYY 60
DB 1 AAPNGTMMQYFEWYLPDDGTLTKVANEANNNSSLGITALLWLPAYKGTSRSDVGYY 60

QY 61 DLYDLGEFNQKGTVRTKYGTAKYQLOAIQAHAAGMQVYADVVDHKGADGTWDAVE 120
DB 61 DLYDLGEFNQKGTVRTKYGTAKYQLOAIQAHAAGMQVYADVVDHKGADGTWDAVE 120

QY 121 VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
DB 121 VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180

QY 181 IGKAWDEVDTEGNYDYLAMYADLMDHPVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240
DB 181 IGKAWDEVDTEGNYDYLAMYADLMDHPVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240

QY 241 FSFPDWLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300
DB 241 FSFPDWLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300

QY 301 SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWPKLAYAFILTRQEG 360
DB 301 SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWPKLAYAFILTRQEG 360

QY 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
DB 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDPPGSGKMMYVKGQHAGKVFDYLTGNRSDTVTINSQGWGEFKVNGGSVSW 480
DB 421 GSGLAALITDPPGSGKMMYVKGQHAGKVFDYLTGNRSDTVTINSQGWGEFKVNGGSVSW 480

QY 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRVAV 514
DB 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRVAV 514

RESULT 15
US-09-381-687-7
; Sequence 7, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OKAZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381, 687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 515
; TYPE: PRT
; ORGANISM: B. stearothermophilus
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US-09-381-687-7

Query Match		98.5%;	Score 2812;	DB 4;	Length 515;
Best Local Similarity		98.8%;	Pred. No. 3e-242;		
Matches 509;		Conservative 1;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	1	AAPFNGTMMQYFEWYLPDDGTLTKVANEANNLSSLGITALLWLPAYKGTSRSDVGYGVY	60		
Db	1	AAPFNGTMMQYFEWYLPDDGTLTKVANEANNLSSLGITALLWLPAYKGTSRSDVGYGVY	60		
Qy	61	DLVDLGEFNKGTVRTKYGTGAQVLOAIQAAHAGMOVYADVDFDHKGADGTEWDAVE	120		
Db	61	DLVDLGEFNKGTVRTKYGTGAQVLOAIQAAHAGMOVYADVDFDHKGADGTEWDAVE	120		
Qy	121	VNFSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKWYHFDGVDWDESRKLSRIYKFRG	180		
Db	121	VNFSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKWYHFDGVDWDESRKLSRIYKFRG	180		
Qy	181	IGKAWDEVDTEGNGYDYLAVDLMDHPVVTTELKNWGWYVNTTNIIDGFRDLDAVKHIK	240		
Db	181	IGKAWDEVDTEGNGYDYLAVDLMDHPVVTTELKNWGWYVNTTNIIDGFRDLDAVKHIK	240		
Qy	241	FSFPDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK	300		
Db	241	FSFPDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK	300		
Qy	301	SGGAFDMRTILMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG	360		
Db	301	SGGAFDMRTILMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG	360		
Qy	361	YPCVFYGDYIGIPQYNIPLSKIDPLLIARRDYAYCTQHDYLDHSDIIGWTREGGTEKP	420		
Db	361	YPCVFYGDYIGIPQYNIPLSKIDPLLIARRDYAYCTQHDYLDHSDIIGWTREGVTEKP	420		
Qy	421	GSGLAALITDGPCKGKMYVKGQHAGKVFDLTGNRSDDTVTINSDGWGEFKVNGGVSVM	480		
Db	421	GSGLAALITDGPCKGKMYVKGQHAGKVFDLTGNRSDDTVTINSDGWGEFKVNGGVSVM	480		
Qy	481	VPRKTTVSTIARPIITTRPWTGEFVRWTEPRLVAMP	515		
Db	481	VPRKTTVSTIARPIITTRPWTGEFVRWTEPRLVAMP	515		

Search completed: October 7, 2004, 00:47:08  
Job time : 17.9573 secs

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